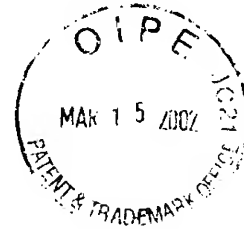


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Sequence Listing



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Botstein, David
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Eaton, Dan L.
Ferrara, Napoleone
Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
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Hillan, Kenneth J.
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<222> 161-163, 187-190 and 253-256

<223> N-glycosylation Sites.

<400> 10

Met	Leu	Phe	Trp	Val	Leu	Gly	Leu	Leu	Ile	Leu	Cys	Gly	Phe	Leu
1				5					10					15

Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20					25					30

Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195

Ala Phe Gly Val	His Val Ser Cys Ile	Glu Pro Gly Leu Phe Lys
200	205	210
Thr Asn Leu Ala	Asp Pro Val Lys Val	Ile Glu Lys Lys Leu Ala
215	220	225
Ile Trp Glu Gln	Leu Ser Pro Asp Ile	Lys Gln Gln Tyr Gly Glu
230	235	240
Gly Tyr Ile Glu	Lys Ser Leu Asp Lys	Leu Lys Gly Asn Lys Ser
245	250	255
Tyr Val Asn Met	Asp Leu Ser Pro Val	Val Glu Cys Met Asp His
260	265	270
Ala Leu Thr Ser	Leu Phe Pro Lys Thr	His Tyr Ala Ala Gly Lys
275	280	285
Asp Ala Lys Ile	Phe Trp Ile Pro Leu	Ser His Met Pro Ala Ala
290	295	300
Leu Gln Asp Phe	Leu Leu Leu Lys Gln	Lys Ala Glu Leu Ala Asn
305	310	315

Pro Lys Ala Val

<210> 11
 <211> 2720
 <212> DNA
 <213> Homo sapiens

<400> 11
 gcgggctggt gacggcgctg cgatggctgc ctgcgagggc aggagaagcg 50
 gagctctcgg ttccctctcag tcggacttcc tgacgcgcgc agtgggcggg 100
 gcccttggg ccgtcgccac cactgtagtc atgtaccac ccgcgcgcgc 150
 gccgctcat cggaacttca tctcggtgac gctgagcttt ggcgagagct 200
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400
 gggttaaaac cagcaaatac accgctctta ccagctctc agaaggcgga 450
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagccctgt 600
 ggatcccgcc ccggaaggag atccgcagag gacagtcctc agctggaggg 650

gggcggtgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700
 gaagtgccea ccaagcctcc cctgccaccg gccaggacac agggcacacc 750
 agtgcattctg aactatcgcc agaaggcgt gattgacgtc ttctgcatg 800
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850
 gtgtccaggt ccttcagtga gtggtttggc ctcggtctca cactgacga 900
 cgcgtggac accatgtgga tcttggtctt gaggaaagaa tttaggaag 950
 ccaggaagtg ggtgtcgaag aagttacact ttgaaaagga cgtggacgtc 1000
 aacctgtttg agagcacgat ccgcattctg ggggggctcc tgagtgccta 1050
 ccacctgtct ggggacagcc tcttctgag gaaagctgag gattttggaa 1100
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 gtgaacatcg gtactggagt tgcccaccgc ccacggtgga cctccgacag 1200
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 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350
 caatacccac agtggcctct tcaccacact gggcgatttc acgctgggcg 1400
 ccagggccga cagctactat gagtacctgc tgaagcagtg gatccagggc 1450
 gggaagcagg agacacagct gctggaagac tacgtggaag ccatcgaggg 1500
 tgtcagaacg cacctgctgc ggcactccga gccagtaag ctacaccttg 1550
 tgggggagct tgcccacggc cgttcagtg ccaagatgga ccacctggtg 1600
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 cagccacatg gagctggccc aggagctcat ggagacttgt taccagatga 1700
 accggcagat ggagacgggg ctgagtcacc agatcgtgca cttcaacctt 1750
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 caacctgctg cggccagaga ccgtggagag cctgttctac ctgtaccgcg 1850
 tcacagggga ccgcaaatac caggactggg gctgggagat tctgcagagc 1900
 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950
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 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gcttatcttg acccctgcct aggggtggatg gctgctggtg tggggaacttc 2150
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 ctccagatgt cccaatcaa gggctcggag gggctgccgt gactccagag 2550
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 cctctggcc gccccgcagg gggcttgag ggctggacgg caagtcctgc 2650
 tagctcacgg gccctccag tggaatgggt cttttcgggt gagataaaag 2700
 ttgatttgct ctaaccgcaa 2720

<210> 12
 <211> 699
 <212> PRT
 <213> Homo sapiens

<220>
 <221> TRANSMEM
 <222> 21-40 and 84-105
 <223> Transmembrane Domain (type II)

<400> 12
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser
 1 5 10 15
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala
 20 25 30
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro
 35 40 45
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr
 50 55 60
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp
 65 70 75
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu
 80 85 90
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala
 95 100 105

Asn	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys	110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val	125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro	140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro	155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly	170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro	185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly	200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg	215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln	230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp	245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly	260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe	275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile	290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser	305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu	320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu	335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn	350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser	365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr	380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe			

395				400				405						
Arg	Glu	Leu	Ser	Arg	Leu	Thr	Gly	Asp	Lys	Lys	Phe	Gln	Glu	Ala
				410					415					420
Val	Glu	Lys	Val	Thr	Gln	His	Ile	His	Gly	Leu	Ser	Gly	Lys	Lys
				425					430					435
Asp	Gly	Leu	Val	Pro	Met	Phe	Ile	Asn	Thr	His	Ser	Gly	Leu	Phe
				440					445					450
Thr	His	Leu	Gly	Val	Phe	Thr	Leu	Gly	Ala	Arg	Ala	Asp	Ser	Tyr
				455					460					465
Tyr	Glu	Tyr	Leu	Leu	Lys	Gln	Trp	Ile	Gln	Gly	Gly	Lys	Gln	Glu
				470					475					480
Thr	Gln	Leu	Leu	Glu	Asp	Tyr	Val	Glu	Ala	Ile	Glu	Gly	Val	Arg
				485					490					495
Thr	His	Leu	Leu	Arg	His	Ser	Glu	Pro	Ser	Lys	Leu	Thr	Phe	Val
				500					505					510
Gly	Glu	Leu	Ala	His	Gly	Arg	Phe	Ser	Ala	Lys	Met	Asp	His	Leu
				515					520					525
Val	Cys	Phe	Leu	Pro	Gly	Thr	Leu	Ala	Leu	Gly	Val	Tyr	His	Gly
				530					535					540
Leu	Pro	Ala	Ser	His	Met	Glu	Leu	Ala	Gln	Glu	Leu	Met	Glu	Thr
				545					550					555
Cys	Tyr	Gln	Met	Asn	Arg	Gln	Met	Glu	Thr	Gly	Leu	Ser	Pro	Glu
				560					565					570
Ile	Val	His	Phe	Asn	Leu	Tyr	Pro	Gln	Pro	Gly	Arg	Arg	Asp	Val
				575					580					585
Glu	Val	Lys	Pro	Ala	Asp	Arg	His	Asn	Leu	Leu	Arg	Pro	Glu	Thr
				590					595					600
Val	Glu	Ser	Leu	Phe	Tyr	Leu	Tyr	Arg	Val	Thr	Gly	Asp	Arg	Lys
				605					610					615
Tyr	Gln	Asp	Trp	Gly	Trp	Glu	Ile	Leu	Gln	Ser	Phe	Ser	Arg	Phe
				620					625					630
Thr	Arg	Val	Pro	Ser	Gly	Gly	Tyr	Ser	Ser	Ile	Asn	Asn	Val	Gln
				635					640					645
Asp	Pro	Gln	Lys	Pro	Glu	Pro	Arg	Asp	Lys	Met	Glu	Ser	Phe	Phe
				650					655					660
Leu	Gly	Glu	Thr	Leu	Lys	Tyr	Leu	Phe	Leu	Leu	Phe	Ser	Asp	Asp
				665					670					675
Pro	Asn	Leu	Leu	Ser	Leu	Asp	Ala	Tyr	Val	Phe	Asn	Thr	Glu	Ala
				680					685					690

His Pro Leu Pro Ile Trp Thr Pro Ala
695

<210> 13
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 13
cgccagaagg gcgtgattga cgtc 24

<210> 14
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 14
ccatccttct tcccagacag gccg 24

<210> 15
<211> 44
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-44
<223> Synthetic construct.

<400> 15
gaagcctgtg tccaggtcct tcagtgaagt gtttggcctc ggtc 44

<210> 16
<211> 1524
<212> DNA
<213> Homo sapiens

<400> 16
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cccatgcgcc gccgcctctc cgcacgatgt tcccctcgcg gaggaagcgc 100
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcgccct 150
ccctcggaag tgttcctgtt tccacctgtt cgtggcctgc ctctcctctgg 200
gtttcttctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cmnagtcg ggggacaagg gcaggagacc tggggccctc cccgtgectg 300
 cccacagag cggcccccctg agcactggga agaagacgca tectggggcc 350
 cccacgectt ggcagtgctg gtgccccttc ggaacgctt cgaggagctc 400
 ctgggtcttcg tgccccacat ggcgcgcttc ctgagcagga agaagatccg 450
 ggcacacatc tacgtgctca accaggttga ccacttcagg ttcaaccggg 500
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 attgacatgc acgacgttga cctgtccct ctcaacgagg agctggacta 600
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 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17
 <211> 327
 <212> PRT
 <213> Homo sapiens
 <220>

<219> sig_peptide
1-42
Signal peptide.

<220> misc_feature
19-25,65-71,247-253,285-291,303-310
<223> N-myristoylation site.

<220>
<221> misc_feature
<222> 27-31
<223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>
<221> TRANSMEM
<222> 29-49
<223> Transmembrane domain (type II).

<220>
<221> misc_feature
<222> 154-158
<223> N-glycosylation site.

<220>
<221> misc_feature
<222> 226-233
<223> Tyrosine kinase phosphorylation site.

<400> 17
Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp
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Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser
20 25 30
Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser
35 40 45
Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala
50 55 60
Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys
65 70 75
Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp
80 85 90
Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe
95 100 105
Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser
110 115 120
Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp
125 130 135
His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu

140	145	150
Asn Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val	Asp
155	160	165
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu	Ala	
170	175	180
Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His		
185	190	195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His		
200	205	210
Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly		
215	220	225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu		
230	235	240
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe		
245	250	255
Arg His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg		
260	265	270
Ile Ala Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly		
275	280	285
Gly Leu Asn Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu		
290	295	300
Ser Val Gly Gly Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp		
305	310	315
Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr Phe Ser		
320	325	

<210> 18
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 18
 gcgaacgctt cgaggagtcc tgg 23

<210> 19
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence

<222> 1-24
<223> Synthetic construct

<400> 19
atgacgggg aagccacatg gtac 24

<210> 20
<211> 46
<212> DNA
<213> Artificial

<210>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 20
cttctctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21
<211> 494
<212> DNA
<213> Homo sapiens

<400> 21
caatgittgc clatccaact cccccaagcc cctttaccta tgcctgctgct 50
aacgctgctg ctgctgctgc tgcctgcttaa aggcctcatgc ttggagtggg 100
gactggtcgg tgcccagaaa gtctctttctg ccactgacgc ccccatcagg 150
gattggggcct tctttccccc ttcttttctg tgtctcctgc ctcatcgggc 200
tgccatgacc tgcagccaag cccagccccc tgggggaaggg gagaaagtgg 250
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtggggtg 300
ggctaggggg gctgccttat ttaaagtggt tgtttatgat tcttatacta 350
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400
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taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> sig_peptide
<222> 1-15
<223> Signal peptide.

<220>
<221> misc_feature
<222> 3-18

<225> Growth factor and cytokines receptors family.

<400> 22

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Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser
          20          25          30

Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser
          35          40          45

Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln
          50          55          60

Ala Gln Pro Arg Gly Gln Gly Glu Lys Val Gly Asp Gly
          65          70

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<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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cccgccccgc agcatggagc caccgggac ccgcggggc cgcgcgcgc 250
cgccgtgtt gctgcgcgc tcgtgttag cgtgtcgcg gctgtggga 300
ggcggcggcg gcggcggcgc cgcggcgctg cccgcggct gcaagcacga 350
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gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctc 550
gaaacaatct tattaagtag atagatccag gtgccttctg gggactgtca 600
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650
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gtggatgcat cgctgggtaa aggagaagaa catcacggt cgggatacca 850

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gaaatgttta tcttaagtca ctgcaggccc aaccagtcac aggcgtgaag 900
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<210> 24
<211> 616
<212> PRT
<213> Homo sapiens

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<221> sig_peptide
<222> 1-33
<223> Signal peptide.

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<220>
<221> TRANSMEM
<222> 13-40
<223> Transmembrane domain (type 11).

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Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly
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Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His
      35             40             45

Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu
      50             55             60

Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro
      65             70             75

Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn
      80             85             90

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Asp	Lys	Ile	Ser	Glu	Leu	Lys	Asn	Gly	Ser	Phe	Ser	Gly	Leu	Ser		95	100	105
Leu	Leu	Glu	Arg	Leu	Asp	Leu	Arg	Asn	Asn	Leu	Ile	Ser	Ser	Ile		110	115	120
Asp	Pro	Gly	Ala	Phe	Trp	Gly	Leu	Ser	Ser	Leu	Lys	Arg	Leu	Asp		125	130	135
Leu	Thr	Asn	Asn	Arg	Ile	Gly	Cys	Leu	Asn	Ala	Asp	Ile	Phe	Arg		140	145	150
Gly	Leu	Thr	Asn	Leu	Val	Arg	Leu	Asn	Leu	Ser	Gly	Asn	Leu	Phe		155	160	165
Ser	Ser	Leu	Ser	Gln	Gly	Thr	Phe	Asp	Tyr	Leu	Ala	Ser	Leu	Arg		170	175	180
Ser	Leu	Glu	Phe	Gln	Thr	Glu	Tyr	Leu	Leu	Cys	Asp	Cys	Asn	Ile		185	190	195
Leu	Trp	Met	His	Arg	Trp	Val	Lys	Glu	Lys	Asn	Ile	Thr	Val	Arg		200	205	210
Asp	Thr	Arg	Cys	Val	Tyr	Pro	Lys	Ser	Leu	Gln	Ala	Gln	Pro	Val		215	220	225
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Leu	Pro	Ser	Phe	Tyr	Met	Thr	Pro	Ser	His	Arg	Gln	Val	Val	Phe		245	250	255
Glu	Gly	Asp	Ser	Leu	Pro	Phe	Gln	Cys	Met	Ala	Ser	Tyr	Ile	Asp		260	265	270
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Thr	Asp	Glu	Ser	Gln	Gly	Ile	Phe	Val	Glu	Lys	Asn	Met	Ile	His		290	295	300
Asn	Cys	Ser	Leu	Ile	Ala	Ser	Ala	Leu	Thr	Ile	Ser	Asn	Ile	Gln		305	310	315
Ala	Gly	Ser	Thr	Gly	Asn	Trp	Gly	Cys	His	Val	Gln	Thr	Lys	Arg		320	325	330
Gly	Asn	Asn	Thr	Arg	Thr	Val	Asp	Ile	Val	Val	Leu	Glu	Ser	Ser		335	340	345
Ala	Gln	Tyr	Cys	Pro	Pro	Glu	Arg	Val	Val	Asn	Asn	Lys	Gly	Asp		350	355	360
Phe	Arg	Trp	Pro	Arg	Thr	Leu	Ala	Gly	Ile	Thr	Ala	Tyr	Leu	Gln		365	370	375
Cys	Thr	Arg	Asn	Thr	His	Gly	Ser	Gly	Ile	Tyr	Pro	Gly	Asn	Pro				

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Thr Arg Val Leu Tyr Met Phe Asn Gln Met Pro Leu Asn Leu Thr 425 430 435		
Asn Ala Val Ala Thr Ala Arg Gln Leu Leu Ala Tyr Thr Val Glu 440 445 450		
Ala Ala Asn Phe Ser Asp Lys Met Asp Val Ile Phe Val Ala Glu 455 460 465		
Met Ile Glu Lys Phe Gly Arg Phe Thr Lys Glu Glu Lys Ser Lys 470 475 480		
Glu Leu Gly Asp Val Met Val Asp Ile Ala Ser Asn Ile Met Leu 485 490 495		
Ala Asp Glu Arg Val Leu Trp Leu Ala Gln Arg Glu Ala Lys Ala 500 505 510		
Cys Ser Arg Ile Val Gln Cys Leu Gln Arg Ile Ala Thr Tyr Arg 515 520 525		
Leu Ala Gly Gly Ala His Val Tyr Ser Thr Tyr Ser Pro Asn Ile 530 535 540		
Ala Leu Glu Ala Tyr Val Ile Lys Ser Thr Gly Phe Thr Gly Met 545 550 555		
Thr Cys Thr Val Phe Gln Lys Val Ala Ala Ser Asp Arg Thr Gly 560 565 570		
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 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24

<223> Synthetic construct

<400> 25

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<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

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<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

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<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

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gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcggg 150

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atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300

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ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

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 <213> Homo sapiens
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 <223> Signal peptide.

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 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln
 35 40 45
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile
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 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala
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 Lys Gly Ser Gln Lys Ser
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<210> 30
 <211> 2128
 <212> DNA
 <213> Homo sapiens

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 tccgtggatt cctctgctaa gaccgtgcc atgccagtga cggtaaccgc 150
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<210> 31
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 31
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 35 40 45
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp
 50 55 60
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys
 65 70 75
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu
 80 85 90
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe
 95 100 105
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr
 110 115 120
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp
 125 130 135
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala
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 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile
 155 160 165
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu
 170 175 180
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn
 185 190 195
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr
 200 205 210

Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn	Leu	
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Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu	
				230					235					240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	
				245					250					255	
Val	Leu	Trp	Pro	Leu	Tyr	Gln	Phe	Asp	Glu	Lys	Tyr	Gly	Gly	Gln	
				260					265					270	
Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His	Ala	Tyr	
				275					280					285	
Tyr	Val	Cys	Ala	Trp	Asp	Arg	Arg	Leu	Ala	Val	Ala	Ile	Leu	Thr	
				290					295					300	
Ala	Ile	Asn	Leu	Leu	Ala	Tyr	Val	Ala	Asp	Leu	Val	His	Ser	Ala	
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 <212> DNA
 <213> Homo sapiens

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taatatataaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala
320 325 330

Glu Pro Glu Glu Gln
335

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct

<400> 34
tgtcctttgt ccagacttc tgtcc 25

<210> 35
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 35
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 36

ttccactcaa tgaggtgagc cactc 25

<210> 37

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-23

<223> Synthetic construct.

<400> 37

ggcgagccct aactatccag gag 23

<210> 38

<211> 39

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-39

<223> Synthetic construct.

<400> 38

ggagatcgct gcgctggcca ggtcctccct gcatggtat 39

<210> 39

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-22

<223> Synthetic construct.

<400> 39

ctgctgcaaa gcgagcctct tg 22

<210> 40

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 40

ggttcctggg cgctctgtta cacaagcaag atacagccag cccacctaa 50

ttttgtttcc ctggcacccct cctgctcagt gcgacattgt cacacttaac 100

ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150

tgataatttca gttcctgatt gtaaataacct cctaagcctg aagcttctgt 200

tactagccat tgtgagcttc agttttcttca tctgcaaaat gggcataata 250

caatctatctc ttgccacatc aagggtattgt tattccttta aaaaaaac 300

aaatgaaag aagcctacaa tgttggcctt agccaaaatt ctgttgattt 350
 caatgttgtt ttattcactt ctatcgggga gccatggaaa agaaaatcaa 400
 tttttaaaca caacacagaa cattgcagaa gtttttaaaa caatggaaaa 450
 ttttttattt tttttggaaa gtgaagcaaa cttaaactca gataaagaaa 500
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 ttttaataca gccacggaat aacagatttc tccagtaact catcagcaga 600
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 ctttgatcca tagctttgtt tctaaagtgc cttggaatgc acctatagca 700
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 ctgataacag ttccattaca gttagcatcc tctcttcaga accaacttct 850
 ccatctgtga ccccttgat agtggaaacca agtggatggc ttaccacaaa 900
 cagtgatagc ttcactgggt ttaccctta tcaagaaaaa acaactctac 950
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 gtgaaaaaag gaaaacggat tcattttccc atcgggcact ttatgacgac 1150
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 ...gtgctgct taaaaactca gtgagaatca tggc 2084

<210> 41
 <211> 134
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr
 1 5 10 15
 Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn
 20 25 30
 Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys
 35 40 45
 Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu
 50 55 60
 Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu
 65 70 75
 Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn
 80 85 90
 Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr
 95 100 105
 Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val
 110 115 120
 Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser
 125 130 135
 Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr
 140 145 150
 Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser
 155 160 165
 Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val
 170 175 180
 Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser
 185 190 195

Arg	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Glu	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42
 <211> 1594
 <212> DNA
 <213> Homo sapiens

<400> 42
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 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200
 tgccaccacg gaaaaagagg gctcctctgg gagatgtatg cttactctct 250
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 ttttgattct gaggatcctg caaattccct tcgtggagga gaggcctaact 400
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 tattcatgac ttgaaaagg gaatgactgc ttacctggac ttgttgctgg 550

gaaatgata tctgatgccc ctcaataactt ctattgttat gctccaaaa 600
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 aatttatgtg gttcgagaag acctagttag tgtggaggaa attcgtgatg 700
 ttugtaacct tgacatcttt atttaccac tttgcaataa cagaaagtc 750
 ttccgcttc gtgcagaga cctcttctg ggttcaaca aacgtgccat 800
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 ccaagatctg tcaagagtaa gaggaacag atagagtgtc ctgggtaata 900
 agaagtcaga gatttacaat atgacttta cattaagggtt tatgggatac 950
 tcaagatatt tactcatgca ttactctat tgettatgct ttaaaaaag 1000
 gaaaaaaaaa aaactacta accactgcaa gctcttgta aattttagtt 1050
 taattggcat tcttgtttt ttgaaactga aattacatga gtttcatttt 1100
 ttcttgcac ttatagggtt tagatttctg aaagcagcat gaatatatca 1150
 cctaacatcc tgacaataaa tccatccgt tgtttttttt gttgtttgt 1200
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 tatcagatct caacattgtt ggtttctttt gtttttcatt ttgtacaact 1350
 ttcttgaatt tagaaattac atctttgcag ttctgttagg tgctctgtaa 1400
 ttaacctgac ttatatgtga acaattttca tgagacagtc atttttaact 1450
 aatgcagtga ttcttttca ctactactg tattgtggaa tgcacaaaat 1500
 tgtgtagggt ctgaatgctg taaggagttt aggttgtatg aattctacaa 1550
 cctataata aattttactc tatacaaaaa aaaaaaaaaa aaaa 1594

<210> 43

<211> 263

<212> PRT

<213> Homo sapiens

<400> 43

Met	Val	Lys	Ile	Ala	Phe	Asn	Thr	Pro	Thr	Ala	Val	Gln	Lys	Glu
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Glu	Ala	Arg	Gln	Asp	Val	Glu	Ala	Leu	Leu	Ser	Arg	Thr	Val	Arg
				20					25					30

Thr	Gln	Ile	Leu	Thr	Gly	Lys	Glu	Leu	Arg	Val	Ala	Thr	Gln	Glu
				35					40					45

Lys	Glu	Gly	Ser	Ser	Gly	Arg	Cys	Met	Leu	Thr	Leu	Leu	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Ser Phe Ile Leu Ala Gly Leu Ile Val	Gly Gly Ala Cys Ile Tyr	
65	70	75
Lys Tyr Phe Met Pro Lys Ser Thr Ile	Tyr Arg Gly Glu Met Cys	
80	85	90
Phe Phe Asp Ser Glu Asp Pro Ala Asn	Ser Leu Arg Gly Gly Glu	
95	100	105
Pro Asn Phe Leu Pro Val Thr Glu Glu	Ala Asp Ile Arg Glu Asp	
110	115	120
Asp Asn Ile Ala Ile Ile Asp Val Pro	Val Pro Ser Phe Ser Asp	
125	130	135
Ser Asp Pro Ala Ala Ile Ile His Asp	Phe Glu Lys Gly Met Thr	
140	145	150
Ala Tyr Leu Asp Leu Leu Leu Gly Asn	Cys Tyr Leu Met Pro Leu	
155	160	165
Asn Thr Ser Ile Val Met Pro Pro Lys	Asn Leu Val Glu Leu Phe	
170	175	180
Gly Lys Leu Ala Ser Gly Arg Tyr Leu	Pro Gln Thr Tyr Val Val	
185	190	195
Arg Glu Asp Leu Val Ala Val Glu Glu	Ile Arg Asp Val Ser Asn	
200	205	210
Leu Gly Ile Phe Ile Tyr Gln Leu Cys	Asn Asn Arg Lys Ser Phe	
215	220	225
Arg Leu Arg Arg Arg Asp Leu Leu Leu	Gly Phe Asn Lys Arg Ala	
230	235	240
Ile Asp Lys Cys Trp Lys Ile Arg His	Phe Pro Asn Glu Phe Ile	
245	250	255
Val Glu Thr Lys Ile Cys Gln Glu		
260		

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<210> 20
<211> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-20
<223> Synthetic construct.

<400> 45
gggaactgct atctgatgcc 20

<210> 46
<211> 26
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-26
<223> Synthetic construct.

<400> 46
caggatctcc tcttgcagtc tgcagc 26

<210> 47
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-28
<223> Synthetic construct.

<400> 47
cttctcgaac cacataagtt tgaggaag 28

<210> 48
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial sequence
<222> 1-25
<223> Synthetic construct.

<400> 48
cacgattccc tccacagcaa ctggg 25

<210> 49
<211> 1969
<212> DNA
<213> Homo sapiens

<400> 49
ggaggaggga gggcgggcag gcgcagccc agagcagccc cgggcacca 50

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 ctctctctct cagcccccag cctcctcacc ctctctgttg tctctctggg 200
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 aatactgtc ttaattttcc tgaagggtgc cccctgttct tagttggtec 1450
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 cccccctg ttgtcacac attgtctggc agcctgtgtc cacaatatte 1750
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 ggcaggaggt cctctccccc atccctccat ctggggctcc cccaacctct 1850
 gcacagctct ccaggtgctg agatataatg caccagcaca ataaaccttt 1900
 attccggcct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950
 aaaaaaaaaa aaaaaaaga 1969

<210> 50
 <211> 283
 <212> PRT
 <213> Homo sapiens

<400> 50
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu
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 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu
 20 25 30
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu
 35 40 45
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro
 50 55 60
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly
 65 70 75
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe
 80 85 90
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala
 95 100 105
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln
 110 115 120
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys
 125 130 135
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe
 140 145 150
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala
 155 160 165

Leu Asp Ser Ser Arg Gln Leu Gln Ala Asp Ile Leu Ala Ala Thr	170	175	180
Gln Asn Leu Lys Ser Pro Thr Arg Ala Ala Leu Gly Gly Gly Asp	185	190	195
Gly Ala Arg Met Val Glu Gly Arg Gly Ala Glu Glu Glu Glu Lys	200	205	210
Gly Ser Gln Glu Gly Asp Gln Glu Val Gln Gly His Gly Val Pro	215	220	225
Val Glu Thr Pro Glu Ala Gln Glu Glu Pro Cys Ser Gly Val Leu	230	235	240
Glu Gly Ala Val Val Ala Gly Glu Gly Gln Gly Glu Leu Glu Gly	245	250	255
Ser Leu Leu Leu Ala Gln Glu Ala Gln Gly Pro Val Gly Pro Pro	260	265	270
Glu Ser Pro Cys Ala Cys Ser Ser Val His Pro Ser Val	275	280	

<210> 51
 <211> 1734
 <212> DNA
 <213> Homo sapiens

<400> 51
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 gcacagagac gcagagcaag ggcqgcaagg aggagaccct ggtgggagga 150
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200
 cctggcctgc ctctgtctgg cctctgcct gggcagtgga gaggttgcc 250
 cctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggcattgg 350
 caaagaggcc ggaggggcag ctggtctctaa agtcagttag gcccttgcc 400
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450
 ggcgagcag atgcttggg caacagggtc ggggaagcag cccatgctct 500
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 acggagcaga tgctgtccgc ggctcctggc aggggggtgcc tggccacagt 600
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 ggagcggcgg aggaaatgga cataaacccg ggtgtgaaaa gccagggaat 1200
 gaagcccgcg ggagcgggga atctgggatt cagggcttca gaggacaggg 1250
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 ccgtgacctc cagacaagga gccaccagat tggatgggag ccccccacact 1550
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 <212> PRT
 <213> Homo sapiens

<400> 52
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 35 40 45
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

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Arg Glu Ala Val Gly Thr Gly Val Arg	Gln Val Pro Gly Phe Gly	
80	85	90
Ala Ala Asp Ala Leu Gly Asn Arg Val	Gly Glu Ala Ala His Ala	
95	100	105
Leu Gly Asn Thr Gly His Glu Ile Gly	Arg Gln Ala Glu Asp Val	
110	115	120
Ile Arg His Gly Ala Asp Ala Val Arg	Gly Ser Trp Gln Gly Val	
125	130	135
Pro Gly His Ser Gly Ala Trp Glu Thr	Ser Gly Gly His Gly Ile	
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Gly Gly Asn Gly Gly Pro Pro Asn Phe	Gly Thr Asn Thr Gln Gly	
200	205	210
Ala Val Ala Gln Pro Gly Tyr Gly Ser	Val Arg Ala Ser Asn Gln	
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245	250	255
Gly Ser Gly Ser Asn Gly Asp Asn Asn	Asn Gly Ser Ser Ser Gly	
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Gly Ser Ser Ser Gly Ser Ser Ser Gly	Ser Ser Ser Gly Gly Ser	
275	280	285
Ser Gly Gly Ser Ser Gly Gly Ser Ser	Gly Asn Ser Gly Gly Ser	
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Arg Gly Asp Ser Gly Ser Glu Ser Ser	Trp Gly Ser Ser Thr Gly	
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 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly
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 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser
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 <213> Homo sapiens

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 <213> Homo sapiens

420 - 54

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Glu	Gly	Pro	Ser	Tyr	Ala	Phe	Glu	Val	Asp	Thr	Val	Ala	Pro	Glu
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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
				65					70					75
Trp	Val	Ser	Gly	Ser	Ser	Gly	Arg	Ser	Gly	Gly	Phe	Met	Arg	Lys
				80					85					90
Ile	Thr	Pro	Thr	Thr	Thr	Thr	Ser	Leu	Gly	Ala	Gln	Pro	Ser	Gln
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Arg	Ile	Gly	Ser	Asn	Cys	Val	Lys	His	Ile	Lys	Ala	Thr	Leu	Val
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				200					205					210
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				215					220					225
Glu	Asn	Ile	Ala	Val	Gly	Leu	Ala	Thr	Glu	Lys	Ala	Cys	Ala	Trp
				230					235					240
Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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 <212> DNA
 <213> Homo sapiens

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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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10

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20

25

30

Asn	Glu	Val	Phe	His	Tyr	Gly	Ser	Leu	Arg	Gly	Arg	Ser	Arg	Arg		35	40	45
Pro	Val	Asn	Leu	Lys	Lys	Trp	Ser	Ile	Thr	Asp	Gly	Tyr	Val	Pro		50	55	60
Ile	Leu	Gly	Asn	Lys	Thr	Leu	Pro	Ser	Arg	Cys	His	Gln	Cys	Val		65	70	75
Ile	Val	Ser	Ser	Ser	Ser	His	Leu	Leu	Gly	Thr	Lys	Leu	Gly	Pro		80	85	90
Glu	Ile	Glu	Arg	Ala	Glu	Cys	Thr	Ile	Arg	Met	Asn	Asp	Ala	Pro		95	100	105
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Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
Glu	Phe	Val	Asn	Arg	Thr	Pro	Glu	Thr	Val	Phe	Ile	Phe	Trp	Gly		140	145	150
Pro	Pro	Ser	Lys	Met	Gln	Lys	Pro	Gln	Gly	Ser	Leu	Val	Arg	Val		155	160	165
Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
Val	Ser	Pro	Gly	Arg	Met	Arg	Gln	Phe	Asp	Asp	Leu	Phe	Arg	Gly		185	190	195
Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
Gly	Trp	Phe	Thr	Met	Val	Ile	Ala	Val	Glu	Leu	Cys	Asp	His	Val		215	220	225
His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
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47 57

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 atagagcggc cgggtggcac tggggccatg gtggctcgt ccagcgacct 2900

ggcctatctg atttgctggg togctctgga ctccatcggt ctccatcctg 2950
 tgccttcct ccccttcctg ttgtggaggg cctggtctaa gcaaaaacat 3000
 cccacagacc tgggttttcc tcgaagtgcc ctccacccct cctgcccgtg 3050
 tactatggtg ccattgggag gactcccagg ccaccaggcc agtggacagc 3100
 cctacctcag tggcatcagt ggacgggccc gtgctaattg gatccacatg 3150
 aatggggct gcccctcggc tgcagtgggc taccggggca tgaagcccca 3200
 ccagcactgc ccaggcgagc ttcagcagca gagtgcacc agcagcctgc 3250
 tqaggcaaac ccattctggc aatggatatg acccccaaaq tcaccagatc 3300
 acgaggggct ccaagtctag cccggacgag ggcctcttct tatacacact 3350
 gcccgacgac tccactcacc agctgctgca gcccacac gactgctgcc 3400
 aacgccagga gcagcctgct gctgtgggcc agtcaggggt gaggagagcc 3450
 cccgacagtc ctgtcctgga agcagtggtg gaccctccat ttcactcagg 3500
 gcccctatgc tgcctgggcc ttgtgccagc tgaagaggtg gacagtcctg 3550
 actcctgcca agtgagtgga ggagactggt gtcccagca ccccgtaggg 3600
 gctacgtag gacaggaacc tggaatgcag ctctccccgg gccactggt 3650
 gcgtgtgtct ttgaaacac cactctcac aatttaggca gaagctgata 3700
 tcccagaaaq actatatatt gtttttttt taaaaaaaaa agaagaaaaa 3750
 agagacagag aaaattgga tttatttttc tattatagcc atatttata 3800
 atttatgcac ttgtaaataa atgtatatgt ttataattc tggagagaca 3850
 taaggagtc taccgctga ggttgagag ggaaaataaa gaagctgcca 3900
 cctaacagga gtcaccagg aaagcaccgc acaggctggc gcgggacaga 3950
 ctctaacct ggggcctctg cagtggcagg cgaggctgca ggaggccac 4000
 agataagctg gcaagaggaa ggatcccagg cacatggttc atcacgagca 4050
 tgagggaaca gcaaggggca cggatcaca gcctggagac acccacacag 4100
 atggctggat ccggtgctac gggaaacatt ttctaagat gccatgaga 4150
 acagaccaag atgtgtacag cactatgagc attaaaaaac cttccagaat 4200
 caataatccg tggcaacata tctctgtaa acaaacact gtaacttcta 4250
 aataaatgtt tagtcttccc tgtaaaa 4277

<210> 58
 <211> 1115

11. FET
 11. Homo sapiens

<400> 58

Met	Leu	Arg	Gly	Thr	Met	Thr	Ala	Trp	Arg	Gly	Met	Arg	Pro	Glu	1	5	10	15
Val	Thr	Leu	Ala	Cys	Leu	Leu	Leu	Ala	Thr	Ala	Gly	Cys	Phe	Ala	20	25	30	
Asp	Leu	Asn	Glu	Val	Pro	Gln	Val	Thr	Val	Gln	Pro	Ala	Ser	Thr	35	40	45	
Val	Gln	Lys	Pro	Gly	Gly	Thr	Val	Ile	Leu	Gly	Cys	Val	Val	Glu	50	55	60	
Pro	Pro	Arg	Met	Asn	Val	Thr	Trp	Arg	Leu	Asn	Gly	Lys	Glu	Leu	65	70	75	
Asn	Gly	Ser	Asp	Asp	Ala	Leu	Gly	Val	Leu	Ile	Thr	His	Gly	Thr	80	85	90	
Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	95	100	105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	110	115	120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	125	130	135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	140	145	150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	155	160	165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	170	175	180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	185	190	195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	200	205	210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	215	220	225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	230	235	240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	245	250	255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	260	265	270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu Leu	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys Met	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu Tyr	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu Ser	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys Glu	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn Ala	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg Ala	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr Gln	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val Gln	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln Asp	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys Leu	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro Arg	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly Glu	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser Ser	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg Pro	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val Val	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr Ile	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg Leu	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn Cys	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly Arg			

Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile Gln	560	565	570
	575	580			585
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro Asp	590	595	600
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr Ile	605	610	615
Phe Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro Arg	620	625	630
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr Lys	635	640	645
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala Ile	650	655	660
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys Gly	665	670	675
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly Glu	680	685	690
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly Tyr	695	700	705
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile Thr	710	715	720
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp Met	725	730	735
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe Tyr	740	745	750
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr Lys	755	760	765
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser His	770	775	780
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe Asn	785	790	795
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu Thr	800	805	810
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro Pro	815	820	825
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu Arg	830	835	840
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu Pro	845	850	855

Tyr	Leu	Ile	Val	Gly	Val	Val	Leu	Gly	Ser	Ile	Val	Leu	Ile	Ile	
				860					865					870	
Val	Thr	Phe	Ile	Pro	Phe	Cys	Leu	Trp	Arg	Ala	Trp	Ser	Lys	Gln	
				875					880					885	
Lys	His	Thr	Thr	Asp	Leu	Gly	Phe	Pro	Arg	Ser	Ala	Leu	Pro	Pro	
				890					895					900	
Ser	Cys	Pro	Tyr	Thr	Met	Val	Pro	Leu	Gly	Gly	Leu	Pro	Gly	His	
				905					910					915	
Gln	Ala	Ser	Gly	Gln	Pro	Tyr	Leu	Ser	Gly	Ile	Ser	Gly	Arg	Ala	
				920					925					930	
Cys	Ala	Asn	Gly	Ile	His	Met	Asn	Arg	Gly	Cys	Pro	Ser	Ala	Ala	
				935					940					945	
Val	Gly	Tyr	Pro	Gly	Met	Lys	Pro	Gln	Gln	His	Cys	Pro	Gly	Glu	
				950					955					960	
Leu	Gln	Gln	Gln	Ser	Asp	Thr	Ser	Ser	Leu	Leu	Arg	Gln	Thr	His	
				965					970					975	
Leu	Gly	Asn	Gly	Tyr	Asp	Pro	Gln	Ser	His	Gln	Ile	Thr	Arg	Gly	
				980					985					990	
Pro	Lys	Ser	Ser	Pro	Asp	Glu	Gly	Ser	Phe	Leu	Tyr	Thr	Leu	Pro	
				995					1000					1005	
Asp	Asp	Ser	Thr	His	Gln	Leu	Leu	Gln	Pro	His	His	Asp	Cys	Cys	
				1010					1015					1020	
Gln	Arg	Gln	Glu	Gln	Pro	Ala	Ala	Val	Gly	Gln	Ser	Gly	Val	Arg	
				1025					1030					1035	
Arg	Ala	Pro	Asp	Ser	Pro	Val	Leu	Glu	Ala	Val	Trp	Asp	Pro	Pro	
				1040					1045					1050	
Phe	His	Ser	Gly	Pro	Pro	Cys	Cys	Leu	Gly	Leu	Val	Pro	Val	Glu	
				1055					1060					1065	
Glu	Val	Asp	Ser	Pro	Asp	Ser	Cys	Gln	Val	Ser	Gly	Gly	Asp	Trp	
				1070					1075					1080	
Cys	Pro	Gln	His	Pro	Val	Gly	Ala	Tyr	Val	Gly	Gln	Glu	Pro	Gly	
				1085					1090					1095	
Met	Gln	Leu	Ser	Pro	Gly	Pro	Leu	Val	Arg	Val	Ser	Phe	Glu	Thr	
				1100					1105					1110	
Pro	Pro	Leu	Thr	Ile											
				1115											

<210> 59
 <211> 25
 <212> DNA
 <213> Artificial

∴ Synthetic construct.

...acaca gcagtcattg cctgc 25

Artificial

223) Synthetic construct.

gcacacgtag cctgtcgttg qagc 24

<213> Artificial

<223> Synthetic construct.

caccccaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<213> Homo sapiens

<223> unknown base

ctgatgcgga gtttcccact cgtggacggc cacaatgacc tgcgccaggt 400
 cctgagacag cgttacaaga atgtgcttca ggatgttacc ctgcgaaatt 450
 tcagccatgg tcagaccagc ctggacaggc tttagagacgg cctcgtgggt 500
 gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550
 cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgct 600
 cctactctga actcgagctt gtgacctcag ctgaaggctt gaacagctct 650
 caaaagctgg cctgcctcat tggcgtgnag ggtgggtcact cactggacag 700
 cagcctctct gtgtgcgca gtttctatgt gctgggggtg cgtacctga 750
 cacttacctt cacctgcagt acaccatggg cagagagttc caccangtct 800
 agacaccaca tgtacaccaa cgtcagcggc ttgacaagct ttggtgagaa 850
 agtagtagag gagttaaac gccctggcat gatgatagat ttgtctatg 900
 catcggacac cttgataaga agggctctgg aagtgtctca ggctcctgtg 950
 atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000
 tcccgatgat atcctgcagc ttctgaagaa cggcggcctc ctgatggtga 1050
 cactgtccat gggggtgctg cagtgcaccc tgccttgcata cgtgtccact 1100
 gtggcagatc actttagcca catcagggca gtcattggat ctgagttcat 1150
 cgggattggg ggaaattatg acgggactgg ccgggttccct caggggctgg 1200
 aggatgtgtc cacataccca gtcttgatac aggagttgct gagtctgasc 1250
 tggagcgagg aagagcttca aggtgtcctt cgtggaaaacc tgcctcgggt 1300
 cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350
 tggaggtga gtttccatat gggcaactga gcacatcctg ccactcccac 1400
 ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450
 gccaaccaat cgggtccctt ggaggtcctc aaatgcctcc ccataccttg 1500
 ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550
 tgcctgacaca gtccgtcccc gcagaggtca ctgtggcaaa gcctcacaaa 1600
 gcccccctctc ctagttcatt cacaagcata tgctgagaat aaacatgcta 1650
 cacatggaaa a 1661

<210> 63
 <211> 487
 <212> PRT
 <213> Homo sapiens

<220>

<221> unsure

<222> 196, 386

<223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
1				5					10					15	
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

260	265	270
Ser Asp Thr Leu Ile Arg Arg Val Leu Glu Val Ser Gln Ala Pro		
275	280	285
Val Ile Phe Ser His Ser Ala Ala Arg Ala Val Cys Asp Asn Leu		
290	295	300
Leu Asn Val Pro Asp Asp Ile Leu Gln Leu Leu Lys Asn Gly Gly		
305	310	315
Ile Val Met Val Thr Leu Ser Met Gly Val Leu Gln Cys Asn Leu		
320	325	330
Leu Ala Asn Val Ser Thr Val Ala Asp His Phe Asp His Ile Arg		
335	340	345
Ala Val Ile Gly Ser Glu Phe Ile Gly Ile Gly Gly Asn Tyr Asp		
350	355	360
Gly Thr Gly Arg Phe Pro Gln Gly Leu Glu Asp Val Ser Thr Tyr		
365	370	375
Pro Val Leu Ile Glu Glu Leu Leu Ser Arg Xaa Trp Ser Glu Glu		
380	385	390
Glu Leu Gln Gly Val Leu Arg Gly Asn Leu Leu Arg Val Phe Arg		
395	400	405
Gln Val Glu Lys Val Arg Glu Glu Ser Arg Ala Gln Ser Pro Val		
410	415	420
Glu Ala Glu Phe Pro Tyr Gly Gln Leu Ser Thr Ser Cys His Ser		
425	430	435
His Leu Val Pro Gln Asn Gly His Gln Ala Thr His Leu Glu Val		
440	445	450
Thr Lys Gln Pro Thr Asn Arg Val Pro Trp Arg Ser Ser Asn Ala		
455	460	465
Ser Pro Tyr Leu Val Pro Gly Leu Val Ala Ala Ala Thr Ile Pro		
470	475	480
Thr Phe Thr Gln Trp Leu Cys		
485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagttcag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50
aacacccaca gatccctcta tgaactgcaat gtgaggtgtc cggcttlgct 100
ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150
cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200
tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250
tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300
gcccattgcca gtgcctggcc atgacgtgga ggccactgac ctgctgtgag 350
agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400
atctacctgt ccgtggtggg tgcctgtgtg ctctacatgg ccttctgat 450
gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500
acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550
tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaggtgac 600

ccagcagcgg tggaagctgc aggtgcagga gcagcggaag acagtcttcg 650
 atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700
 ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750
 ctcccttccc tcggttccag ttctcccttt aaaagcctgt ggcatttttc 800
 ctcttctcc ctaacttlag aaatgttgta cttggctatt ttgattaggg 850
 aagagggatg tggctctga tctctgttgt cttcttgggt ctttgggggt 900
 gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950
 ctcaggagtg galgcgact gtctctcttg gctccactct tgcgccttc 1000
 cagctctgag tcttgggaat gttgttacc ttggaagata aagctgggtc 1050
 ttcaggaaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100
 gttcctttct gcagtggctc ttatcaccac ctccctccca gccccggcgc 1150
 ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200
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 cgctgtcccc tgtgcacttc tcgcactggg gcattggagt cccatgcata 1300
 ctctgctgcc ggtccctca cctgcacttg aggggtctgg gcagtccctc 1350
 ctctccccag tgtccacagt cactgagcca gacggctcgt tggaaacatga 1400
 gactcgaggc tgagcgtgga tctgaacacc acagcccttg tacttgggtt 1450
 gcctcttgtc cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500
 tctcttgtc ttagagttgt gtgtaaatca aggaagccat cattaaattg 1550
 tttattttct ctca 1564

<210> 68
 <211> 183
 <212> PRT
 <213> Homo sapiens

<400> 68
 Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val
 1 5 10 15
 Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys
 20 25 30
 Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn
 35 40 45
 Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu
 50 55 60

Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu	
				65					70					75	
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val	
				80					85					90	
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr	
				95					100					105	
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp	
				110					115					120	
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala	
				125					130					135	
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala	
				140					145					150	
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys	
				155					160					165	
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys	
				170					175					180	

Met Leu Ser

<210> 69
 <211> 3170
 <212> DNA
 <213> Homo sapiens

<400> 69
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50
 agttcatagg gtcttggttc cccgaaccag gaagggttga gggaacacaa 100
 tctgcaagcc cccgcgaccc aagtgagggg ccccggttg gggctctccc 150
 tccctttgca tccccacccc tccgggcttt gcgtcttctt ggggaccccc 200
 tcgcccggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250
 tgctctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300
 tcgcccggca aactcaactc catcaagtc tctctgggcg gggagacgcc 350
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400
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 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25				30	

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40				45	

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
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Cys Gln Lys Ile

<210> 71
 <211> 1809
 <212> DNA
 <213> Homo sapiens

<400> 71
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 ctcccttta acttttatg tcagaatgag gaaggatagc tqcatttatt 200

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 aaacttctg atgtgtttta aagccttggg cagaaattct gtattgttga 350
 ggatttggtc ttttatcccc cttttaaagt catccgtcct tggctcagga 400
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 ttggaccag ttgaaagctc cgagtttggg ccagtttacc accaccccaa 500
 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550
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 gccgggtgtg gtggcggggc gtgcctgtaa tccagctac ttgggaggct 1750
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 ctg taaqa 1809

<210> 72
 <211> 363
 <212> PRT
 <213> Homo sapiens

<400> 72
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 20 25 30
 Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser
 35 40 45
 Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr
 50 55 60
 Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr
 65 70 75
 Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val
 80 85 90
 Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val
 95 100 105
 Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val
 110 115 120
 Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys
 125 130 135
 Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys
 140 145 150
 Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser
 155 160 165
 Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg
 170 175 180
 Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro
 185 190 195
 Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu
 200 205 210
 Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro
 215 220 225

Val	Leu	Glu	Asn	Ser	Asn	Gln	Ile	Pro	Ile	Ser	Leu	Tyr	Ser	Lys
				230					235					240
Leu	Leu	Ser	Glu	Pro	Leu	Asn	Thr	Ser	Leu	Ser	Met	Thr	Ser	Ala
				245					250					255
Val	Gln	Asn	Ser	Thr	Tyr	Thr	Thr	Ser	Val	Ile	Thr	Ser	Cys	Ser
				260					265					270
Leu	Thr	Ser	Ser	Ser	Leu	Asn	Ser	Ala	Ser	Pro	Val	Ala	Met	Ser
				275					280					285
Ser	Ser	Tyr	Asp	Gln	Ser	Ser	Val	His	Asn	Arg	Ile	Pro	Tyr	Gln
				290					295					300
Ser	Pro	Val	Ser	Ser	Ser	Glu	Ser	Ala	Pro	Gly	Thr	Ile	Met	Asn
				305					310					315
Gly	His	Gly	Gly	Gly	Arg	Ser	Gln	Gln	Thr	Leu	Asp	Ser	Lys	Tyr
				320					325					330
Ser	Ser	Lys	Leu	Leu	Leu	Ser	Trp	Leu	Val	Pro	Thr	Lys	Gln	Arg
				335					340					345
Lys	Arg	Ile	Ala	His	Val	Met	Trp	Lys	Thr	Pro	Val	Gly	Gln	Trp
				350					355					360

Leu Ile Arg

<210> 73
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 73
 aattcatggc aaatatttcc cttccc 26

<210> 74
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 74
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<210> 75
 <211> 50

<21> RNA
<211> Artificial

<212> Artificial sequence
<213> 1-50
<214> Synthetic construct

<41> 75
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<21> 76
<211> 1989
<212> DNA
<213> Homo sapiens

<400> 76
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 ccactctcag cccccacat ttgcatctgc tgggtggacct gccaccatca 1950
 caataaagtc cccatctgat ttttaaaaaa aaaaaaaaaa 1989

<210> 77

<211> 341

<212> PRT

<213> Homo sapiens

<400> 77

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Gln	Ser	Ser	Ala	Val	Leu	Leu	His	Ser	Ala	Val	Glu	Glu	Thr	Asp
				20					25					30

Ala	Gly	Leu	Tyr	Thr	Cys	Asn	Leu	His	His	His	Tyr	Cys	His	Leu
				35					40					45

Tyr	Glu	Ser	Leu	Ala	Val	Arg	Leu	Glu	Val	Thr	Asp	Gly	Pro	Pro
				50					55					60

Ala	Thr	Pro	Ala	Tyr	Trp	Asp	Gly	Glu	Lys	Glu	Val	Leu	Ala	Val
				65					70					75

Ala	Arg	Gly	Ala	Pro	Ala	Leu	Leu	Thr	Cys	Val	Asn	Arg	Gly	His	80	85	90
Val	Trp	Thr	Asp	Arg	His	Val	Glu	Glu	Ala	Gln	Gln	Val	Val	His	95	100	105
Trp	Asp	Arg	Gln	Pro	Pro	Gly	Val	Pro	His	Asp	Arg	Ala	Asp	Arg	110	115	120
Leu	Leu	Asp	Leu	Tyr	Ala	Ser	Gly	Glu	Arg	Arg	Ala	Tyr	Gly	Pro	125	130	135
Leu	Phe	Leu	Arg	Asp	Arg	Val	Ala	Val	Gly	Ala	Asp	Ala	Phe	Glu	140	145	150
Arg	Gly	Asp	Phe	Ser	Leu	Arg	Ile	Glu	Pro	Leu	Glu	Val	Ala	Asp	155	160	165
Glu	Gly	Thr	Tyr	Ser	Cys	His	Leu	His	His	His	Tyr	Cys	Gly	Leu	170	175	180
His	Glu	Arg	Arg	Val	Phe	His	Leu	Thr	Val	Ala	Glu	Pro	His	Ala	185	190	195
Glu	Pro	Pro	Pro	Arg	Gly	Ser	Pro	Gly	Asn	Gly	Ser	Ser	His	Ser	200	205	210
Gly	Ala	Pro	Gly	Pro	Asp	Pro	Thr	Leu	Ala	Arg	Gly	His	Asn	Val	215	220	225
Ile	Asn	Val	Ile	Val	Pro	Glu	Ser	Arg	Ala	His	Phe	Phe	Gln	Gln	230	235	240
Leu	Gly	Tyr	Val	Leu	Ala	Thr	Leu	Leu	Leu	Phe	Ile	Leu	Leu	Leu	245	250	255
Val	Thr	Val	Leu	Leu	Ala	Ala	Arg	Arg	Arg	Arg	Gly	Gly	Tyr	Glu	260	265	270
Tyr	Ser	Asp	Gln	Lys	Ser	Gly	Lys	Ser	Lys	Gly	Lys	Asp	Val	Asn	275	280	285
Leu	Ala	Glu	Phe	Ala	Val	Ala	Ala	Gly	Asp	Gln	Met	Leu	Tyr	Arg	290	295	300
Ser	Glu	Asp	Ile	Gln	Leu	Asp	Tyr	Lys	Asn	Asn	Ile	Leu	Lys	Glu	305	310	315
Arg	Ala	Glu	Leu	Ala	His	Ser	Pro	Leu	Pro	Ala	Lys	Tyr	Ile	Asp	320	325	330
Leu	Asp	Lys	Gly	Phe	Arg	Lys	Glu	Asn	Cys	Lys					335	340	

<210> 78
 <211> 2243
 <212> DNA
 <213> Homo sapiens

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 gaagggtgtc ccttggaatg gaagtcctcc ggcattggtc gtctcaggc 1950
 ccaagactca agtgtgcaca gacctctgtt ttctgcgggt gaacaactgc 2000
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 ggctgggtt ttcaaaaaaa gagggatcct catgacctgg tggctatagg 2150
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<210> 79

<211> 475

<212> PRT

<213> Homo sapiens

<400> 79

Met	Ala	Val	Val	Ser	Glu	Asp	Asp	Phe	Gln	His	Ser	Ser	Asn	Ser	1	5	10	15
Thr	Tyr	Gly	Thr	Thr	Ser	Ser	Ser	Leu	Arg	Ala	Asp	Gln	Glu	Ala	20	25	30	
Leu	Leu	Glu	Lys	Leu	Leu	Asp	Arg	Pro	Pro	Pro	Gly	Leu	Gln	Arg	35	40	45	
Pro	Glu	Asp	Arg	Phe	Cys	Gly	Thr	Tyr	Ile	Ile	Phe	Phe	Ser	Leu	50	55	60	
Gly	Ile	Gly	Ser	Leu	Leu	Pro	Trp	Asn	Phe	Phe	Ile	Thr	Ala	Lys	65	70	75	
Glu	Tyr	Trp	Met	Phe	Lys	Leu	Arg	Asn	Ser	Ser	Ser	Pro	Ala	Thr	80	85	90	
Gly	Glu	Asp	Pro	Glu	Gly	Ser	Asp	Ile	Leu	Asn	Tyr	Phe	Glu	Ser	95	100	105	

Val	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val		110	115	120
Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val			125	130	135
Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr			140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe		155	160	165
Arg	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr		170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met		185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr		200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp		215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe		230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu		245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe		260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser		275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro		290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val		305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile		320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe		335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu		350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn		365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile		380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys				

	395		400		405									
Pro	Val	Val	Phe	Gln	Ser	Asp	Val	Tyr	Pro	Ala	Leu	Leu	Ser	Ser
				410					415				420	
Leu	Leu	Gly	Leu	Ser	Asn	Gly	Tyr	Leu	Ser	Thr	Leu	Ala	Leu	Leu
				425					430				435	
Pyr	Gly	Pro	Lys	Ile	Val	Pro	Arg	Glu	Leu	Ala	Glu	Ala	Thr	Gly
				440					445				450	
Val	Val	Met	Ser	Phe	Tyr	Val	Cys	Leu	Gly	Leu	Thr	Leu	Gly	Ser
				455					460				465	
Ala	Cys	Ser	Thr	Leu	Leu	Val	His	Leu	Ile					
				470				475						

<210> 80
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 80
 ttttgcggtc accattgtct gc 22

<210> 81
 <211> 23
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Artificial sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 81
 cgtaggtgac acagaagccc agg 23

<210> 82
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 82
 tacggcatga ccggctcctt tctatgagg aactcccagg cactgatat 49

<210> 83
 <211> 1844

<212> DNA
<213> Homo sapiens

<400> 83

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aaggtgaac gcagccaaga ccccttcgag aaatgcctgc aggatcctga 200
ctatgagcag ctgctcaagg tggtagctg ggggtcaat cggacctga 250
agccccagag ggtgatttg gttggcctg gtgtggcgg gctggtggc 300
gccaaagtgc tcagcgatgc tggacacaag gtcaccatcc tggaggcaga 350
taacaggatc gggggccgca tcttcacctc ccgggaccag aacacgggt 400
ggattgggga gctgggagcc atgcgcctgc ccagctctca caggatctc 450
cacaagctct gccagggcct ggggtcaac ctgaccaagt tcaccagta 500
cgacaagaac acgtggacgg aggtgcacga agtgaagctg cgcactatg 550
tggtaggaa ggtgcccag aagctgggt acgccttgcg tcccaggaa 600
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ccgccttgag ccgggaagag gcgttgcgt tggcgtcga cgacgtggcg 1350

gatttgcacg ggccctgtcgt gcgcacagctc tgggacggca cggcgctcgt 1430
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 cgcctctact ttgcgggca gcacacggcc taccgcacg gctgggtgga 1550
 gacggcggtc aagtcgggc tgcgcgcgc catcaagatc aacagccgga 1600
 aggggcctgc atcggacacg gccagcccg aggggcacgc atctgacatg 1650
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 gqcaaaggaa gaaggcagcc acctccagt ccaaggccag ttatctctcc 1750
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84
 <211> 567
 <212> PRT
 <213> Homo sapiens

<400> 84
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 20 25 30
 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu
 35 40 45
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln
 50 55 60
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala
 65 70 75
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala
 80 85 90
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn
 95 100 105
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser
 110 115 120
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu
 125 130 135
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His
 140 145 150
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys
 155 160 165

Leu Gly Tyr Ala	Leu Arg Pro Gln Glu	Lys Gly His Ser Pro	Glu
170	175		180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln	Ala Leu Lys Asp Leu	Lys
185	190		195
Ala Leu Gly Cys	Arg Lys Ala Met Lys	Lys Phe Glu Arg His	Thr
200	205		210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly	Asn Leu Ser Arg Pro	Ala
215	220		225
Val Gln Leu Leu	Gly Asp Val Met Ser	Glu Asp Gly Phe Phe	Tyr
230	235		240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala	His Ser Cys Leu Ser	Asp
245	250		255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly	Gly Trp Asp Leu Leu	Pro
260	265		270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly	Leu Val Leu Leu Asn	Ala
275	280		285
Pro Val Val Ala	Met Thr Gln Gly Pro	His Asp Val His Val	Gln
290	295		300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn	Leu Lys Val Leu Lys	Ala
305	310		315
Asp Val Val Leu	Leu Thr Ala Ser Gly	Pro Ala Val Lys Arg	Ile
320	325		330
Thr Phe Ser Pro	Pro Leu Pro Arg His	Met Gln Glu Ala Leu	Arg
335	340		345
Arg Leu His Tyr	Val Pro Ala Thr Lys	Val Phe Leu Ser Phe	Arg
350	355		360
Arg Pro Phe Trp	Arg Glu Glu His Ile	Glu Gly Gly His Ser	Asn
365	370		375
Thr Asp Arg Pro	Ser Arg Met Ile Phe	Tyr Pro Pro Pro Arg	Glu
380	385		390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr	Trp Ser Asp Ala Ala	Ala
395	400		405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu	Ala Leu Arg Leu Ala	Leu
410	415		420
Asp Asp Val Ala	Ala Leu His Gly Pro	Val Val Arg Gln Leu	Trp
425	430		435
Asp Gly Thr Gly	Val Val Lys Arg Trp	Ala Glu Asp Gln His	Ser
440	445		450
Gln Gly Gly Phe	Val Val Gln Pro Pro	Ala Leu Trp Gln Thr	Glu

	455		460		465
Lys Asp Asp Trp Thr Val Pro Tyr Gly Arg Ile Tyr Phe Ala Gly					
	470		475		480
Glu His Thr Ala Tyr Pro His Gly Trp Val Glu Thr Ala Val Lys					
	485		490		495
Ser Ala Leu Arg Ala Ala Ile Lys Ile Asn Ser Arg Lys Gly Pro					
	500		505		510
Ala Ser Asp Thr Ala Ser Pro Glu Gly His Ala Ser Asp Met Glu					
	515		520		525
Gly Gln Gly His Val His Gly Val Ala Ser Ser Pro Ser His Asp					
	530		535		540
Leu Ala Lys Glu Glu Gly Ser His Pro Pro Val Gln Gly Gln Leu					
	545		550		555
Ser Leu Gln Asn Thr Thr His Thr Arg Thr Ser His					
	560		565		

<210> 85
 <211> 3316
 <212> DNA
 <213> Homo sapiens

<400> 85
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 ctctggggccg gcctttctgcc tgcattggaag ctctgaagcc accctgtctc 100
 tggaggaacc acgagcagag gaagaaggac agggactcgt gtggcaggaa 150
 gaactcagag ccgggaagcc cccattcact agaagcactg agagatgcag 200
 cccctcgcg gggctctgaat ttctctctgc tgttcacaaa gatgcctttt 250
 atctttaact ttttgttttc cccacttcag accccggcgt tgatctgcat 300
 cctgacattt ggagctgcca tcttcttggt gctgatcacc agacctcaac 350
 ccgtcttacc tcttcttgac ctgaacaatc agtctgtggg aattgaggga 400
 ggagcacgga aggggggttt ccagaagaac aatgacctaa caagttgctg 450
 cttctcagat gccaaagacta tgtatgaggt ttccaaaga ggactcgtctg 500
 tgtctgacaa tggggccctgc ttgggatata gaaaaccaa ccagccctac 550
 agatggctat cttacaaaca ggtgtctgat agagcagagt acctgggttc 600
 ctgtctcttg cataaagggt ataatcctc accagaccag tttgtcggca 650
 tctttgctca gaataggcca gactggatca tctccgaatt ggcttggtac 700
 acgtactcta tggtagctgt acctctgtat gacaccttg gaccagaagc 750

catcgtacat attgtcaaca aggcctgatat cggcatgggtg atctgtgaca 800
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 ccgagcctga aggtgatcat ccttatggac ccccttgatg atgaacctgaa 900
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 gacctgagcg tcctctgctt caccagtggg accacagggtg accccaaagg 1050
 agccatgata acccatcaaa atattgtttc aaatgctgct gcctttctca 1100
 aatgtgtgga gcatgcttat gagcccactc ctgatgaltg ggccatatcc 1150
 tacctccctc tggctcatat gtttgagaag attgtacagg ctgttggtga 1200
 cagctgtgga gccagagttg gattcttcca aggggatatt cggttgctgg 1250
 ctgacgacat gaagactttg aagcccacat tgtttccgcg ggtgcctcga 1300
 ctccctaaca ggatctaaga taaggtaaaa aatgaggcca agacaccctt 1350
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 aagatccagg acagcctggg cggaagggtt cgtgtaattg tcactggagc 1500
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 gcaccagaga agatagaaaa tatctacaac aggagtcaac cagtgttaca 1950
 aatttttgta cagggggaga gcttacggtc atccttagta ggagtgggtg 2000
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 ggctcctttg aggaactgtg ccaaaaccaa gttgtaaggg aagccatttt 2100
 agaagacttg cagaaaattg ggaaagaaag tggccttaaa acttttgaac 2150
 aggtcaaaagc catttttctt catccagagc cattttccat tgaaaatggg 2200

ctcttgacac caacattgaa agcaaaagcga ggagagcttt ccaaatactt 2250
 tgggacccaa attgacagcc tgtatgagca catccaggat taggataagg 2300
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<210> 86

<211> 739

<212> PRT

<213> Homo sapiens

<400> 86

Met	Asp	Ala	Leu	Lys	Pro	Pro	Cys	Leu	Trp	Arg	Asn	His	Glu	Arg
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Gly	Lys	Lys	Asp	Arg	Asp	Ser	Cys	Gly	Arg	Lys	Asn	Ser	Glu	Pro
			20						25					30

Gly	Ser	Pro	His	Ser	Leu	Glu	Ala	Leu	Arg	Asp	Ala	Ala	Pro	Ser	
				35					40					45	
Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile	
				50					55					60	
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys	
				65					70					75	
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg	
				80					85					90	
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val	
				95					100					105	
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn	
				110					115					120	
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu	
				125					130					135	
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu	
				140					145					150	
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys	
				155					160					165	
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His	
				170					175					180	
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala	
				185					190					195	
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr	
				200					205					210	
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu	
				215					220					225	
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile	
				230					235					240	
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu	
				245					250					255	
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro	
				260					265					270	
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu	
				275					280					285	
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe	
				290					295					300	
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys	
				305					310					315	
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr	

	320		325		330
His Gln Asn Ile Val Ser Asn Ala Ala Ala Phe Leu Lys Cys Val	335		340		345
Glu His Ala Tyr Glu Pro Thr Pro Asp Asp Val Ala Ile Ser Tyr	350		355		360
Leu Pro Leu Ala His Met Phe Glu Arg Ile Val Gln Ala Val Val	365		370		375
Pyr Ser Cys Gly Ala Arg Val Gly Phe Phe Gln Gly Asp Ile Arg	380		385		390
Leu Leu Ala Asp Asp Met Lys Thr Leu Lys Pro Thr Leu Phe Pro	395		400		405
Ala Val Pro Arg Leu Leu Asn Arg Ile Tyr Asp Lys Val Gln Asn	410		415		420
Glu Ala Lys Thr Pro Leu Lys Lys Phe Leu Leu Lys Leu Ala Val	425		430		435
Ser Ser Lys Phe Lys Glu Leu Gln Lys Gly Ile Ile Arg His Asp	440		445		450
Ser Phe Trp Asp Lys Leu Ile Phe Ala Lys Ile Gln Asp Ser Leu	455		460		465
Gly Gly Arg Val Arg Val Ile Val Thr Gly Ala Ala Pro Met Ser	470		475		480
Thr Ser Val Met Thr Phe Phe Arg Ala Ala Met Gly Cys Gln Val	485		490		495
Tyr Glu Ala Tyr Gly Gln Thr Glu Cys Thr Gly Gly Cys Thr Phe	500		505		510
Thr Leu Pro Gly Asp Trp Thr Ser Gly His Val Gly Val Pro Leu	515		520		525
Ala Cys Asn Tyr Val Lys Leu Glu Asp Val Ala Asp Met Asn Tyr	530		535		540
Phe Thr Val Asn Asn Glu Gly Glu Val Cys Ile Lys Gly Thr Asn	545		550		555
Val Phe Lys Gly Tyr Leu Lys Asp Pro Glu Lys Thr Gln Glu Ala	560		565		570
Leu Asp Ser Asp Gly Trp Leu His Thr Gly Asp Ile Gly Arg Trp	575		580		585
Leu Pro Asn Gly Thr Leu Lys Ile Ile Asp Arg Lys Lys Asn Ile	590		595		600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile Ala Pro Glu Lys Ile Glu	605		610		615

Leu	Ile	Tyr	Asn	Arg	Ser	Gln	Pro	Val	Leu	Gln	Ile	Phe	Val	His
				620					625					630
Glu	Glu	Ser	Leu	Arg	Ser	Ser	Leu	Val	Gly	Val	Val	Val	Pro	Asp
				635					640					645
Thr	Asp	Val	Leu	Pro	Ser	Phe	Ala	Ala	Lys	Leu	Gly	Val	Lys	Gly
				650					655					660
Ser	Phe	Glu	Glu	Leu	Cys	Gln	Asn	Gln	Val	Val	Arg	Glu	Ala	Ile
				665					670					675
Leu	Glu	Asp	Leu	Gln	Lys	Ile	Gly	Lys	Glu	Ser	Gly	Leu	Lys	Thr
				680					685					690
Phe	Glu	Gln	Val	Lys	Ala	Ile	Phe	Leu	His	Pro	Glu	Pro	Phe	Ser
				695					700					705
Ile	Glu	Asn	Gly	Leu	Leu	Thr	Pro	Thr	Leu	Lys	Ala	Lys	Arg	Gly
				710					715					720
Glu	Leu	Ser	Lys	Tyr	Phe	Arg	Thr	Gln	Ile	Asp	Ser	Leu	Tyr	Glu
				725					730					735

His Ile Gln Asp

<210> 87
 <211> 2725
 <212> DNA
 <213> Homo sapiens

<400> 87
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 gcccgagcgg ggcggggggc ccctaagcca ttctgaagt catgggctgg 100
 ccaggacatt ggtgaccgc caatccggt tggacgactg gaagcccagc 150
 cccctcatca agcccttttg ggtcggaag aagcggagct ggtaccttac 200
 ctggaagtat aaactgacaa accagcgggc cctgcggaga ttctgtcaga 250
 caggggccgt gcttttctg ctggtgactg tcattgtcaa tatcaagttg 300
 atcctggaca ctggcgagc catcagtga gccaatgaag acccagagcc 350
 agagcaagac tatgatgagg ccctaggccg cctggagccc ccacggcgca 400
 gaggcagtgg tccccggcgg gtctggacg tagaggtgta ttcaagtcgc 450
 agcaaagtat atgtggcagt ggatggcacc acggtgctgg aggatgaggc 500
 ccgggagcag ggcgggggca tccatgtcat tgtctcaac caggccacgg 550
 gccacgtgat ggcaaacgt gtgtttgaca cgtactcacc tcatgaggat 600
 gaggcgatgg tctattct caacatggt ggcggggcc gactgtcat 650

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 gacacagagc tgaaccgtcg ccgcgggcgc ttctgcagca aagttgaggg 950
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 ctgaccact cccagacaac aaggctcctc atgtgcctgt ggcctgcatt 1050
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 agcccagggg gtgtctcctc agatgataac agttttcatt gacggctact 1150
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 aaaaaaaaaa aaaaaaaaaa aaaaa 2725

<210> 88
 <211> 660
 <212> PRT
 <213> Homo sapiens

<400> 88
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 35 40 45
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp
 50 55 60
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu
 65 70 75
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg
 80 85 90
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser
 95 100 105
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu
 110 115 120
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val
 125 130 135

Asn	Gln	Ala	Thr	Gly	His	Val	Met	Ala	Lys	Arg	Val	Phe	Asp	
			140					145					150	
Thr	Tyr	Ser	Pro	His	Glu	Asp	Glu	Ala	Met	Val	Leu	Phe	Leu	Asn
			155					160					165	
Met	Val	Ala	Pro	Gly	Arg	Val	Leu	Ile	Cys	Thr	Val	Lys	Asp	Glu
			170					175					180	
Gly	Ser	Phe	His	Leu	Lys	Asp	Thr	Ala	Lys	Ala	Leu	Leu	Arg	Ser
			185					190					195	
Leu	Gly	Ser	Gln	Ala	Gly	Pro	Ala	Leu	Gly	Trp	Arg	Asp	Thr	Trp
			200					205					210	
Ala	Phe	Val	Gly	Arg	Lys	Gly	Gly	Pro	Val	Phe	Gly	Glu	Lys	His
			215					220					225	
Ser	Lys	Ser	Pro	Ala	Leu	Ser	Ser	Trp	Gly	Asp	Pro	Val	Leu	Leu
			230					235					240	
Lys	Thr	Asp	Val	Pro	Leu	Ser	Ser	Ala	Glu	Glu	Ala	Glu	Cys	His
			245					250					255	
Trp	Ala	Asp	Thr	Glu	Leu	Asn	Arg	Arg	Arg	Arg	Arg	Phe	Cys	Ser
			260					265					270	
Lys	Val	Glu	Gly	Tyr	Gly	Ser	Val	Cys	Ser	Cys	Lys	Asp	Pro	Thr
			275					280					285	
Pro	Ile	Glu	Phe	Ser	Pro	Asp	Pro	Leu	Pro	Asp	Asn	Lys	Val	Leu
			290					295					300	
Asn	Val	Pro	Val	Ala	Val	Ile	Ala	Gly	Asn	Arg	Pro	Asn	Tyr	Leu
			305					310					315	
Tyr	Arg	Met	Leu	Arg	Ser	Leu	Leu	Ser	Ala	Gln	Gly	Val	Ser	Pro
			320					325					330	
Gln	Met	Ile	Thr	Val	Phe	Ile	Asp	Gly	Tyr	Tyr	Glu	Glu	Pro	Met
			335					340					345	
Asp	Val	Val	Ala	Leu	Phe	Gly	Leu	Arg	Gly	Ile	Gln	His	Thr	Pro
			350					355					360	
Ile	Ser	Ile	Lys	Asn	Ala	Arg	Val	Ser	Gln	His	Tyr	Lys	Ala	Ser
			365					370					375	
Leu	Thr	Ala	Thr	Phe	Asn	Leu	Phe	Pro	Glu	Ala	Lys	Phe	Ala	Val
			380					385					390	
Val	Leu	Glu	Glu	Asp	Leu	Asp	Ile	Ala	Val	Asp	Phe	Phe	Ser	Phe
			395					400					405	
Leu	Ser	Gln	Ser	Ile	His	Leu	Leu	Glu	Glu	Asp	Asp	Ser	Leu	Tyr
			410					415					420	
Cys	Ile	Ser	Ala	Trp	Asn	Asp	Gln	Gly	Tyr	Glu	His	Thr	Ala	Glu

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Asp	Pro	Ala	Leu	Leu	Tyr	Arg	Val	Glu	Thr	Met	Pro	Gly	Leu	Gly
			440						445					450
Trp	Val	Leu	Arg	Arg	Ser	Leu	Tyr	Lys	Glu	Glu	Leu	Glu	Pro	Lys
			455						460					465
Trp	Pro	Thr	Pro	Glu	Lys	Leu	Trp	Asp	Trp	Asp	Met	Trp	Met	Arg
			470						475					480
Met	Pro	Glu	Gln	Arg	Arg	Gly	Arg	Glu	Cys	Ile	Ile	Pro	Asp	Val
			485						490					495
Ser	Arg	Ser	Tyr	His	Phe	Gly	Ile	Val	Gly	Leu	Asn	Met	Asn	Gly
			500						505					510
Tyr	Phe	His	Glu	Ala	Tyr	Phe	Lys	Lys	His	Lys	Phe	Asn	Thr	Val
			515						520					525
Pro	Gly	Val	Gln	Leu	Arg	Asn	Val	Asp	Ser	Leu	Lys	Lys	Glu	Ala
			530						535					540
Tyr	Glu	Val	Glu	Val	His	Arg	Leu	Leu	Ser	Glu	Ala	Glu	Val	Leu
			545						550					555
Asp	His	Ser	Lys	Asn	Pro	Cys	Glu	Asp	Ser	Phe	Leu	Pro	Asp	Thr
			560						565					570
Glu	Gly	His	Thr	Tyr	Val	Ala	Phe	Ile	Arg	Met	Glu	Lys	Asp	Asp
			575						580					585
Asp	Phe	Thr	Thr	Trp	Thr	Gln	Leu	Ala	Lys	Cys	Leu	His	Ile	Trp
			590						595					600
Asp	Leu	Asp	Val	Arg	Gly	Asn	His	Arg	Gly	Leu	Trp	Arg	Leu	Phe
			605						610					615
Arg	Lys	Lys	Asn	His	Phe	Leu	Val	Val	Gly	Val	Pro	Ala	Ser	Pro
			620						625					630
Tyr	Ser	Val	Lys	Lys	Pro	Pro	Ser	Val	Thr	Pro	Ile	Phe	Leu	Glu
			635						640					645
Pro	Pro	Pro	Lys	Glu	Glu	Gly	Ala	Pro	Gly	Ala	Pro	Glu	Gln	Thr
			650						655					660

<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

atgggcacaaa cgtgtgtttg acacg 25
 <210> 90
 <211> 22
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-22
 <223> Synthetic construct.

 <400> 90
 cctcaaccag gccacggccc ac 22

 <210> 91
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 91
 cccaggcaga gatgcagtac aggc 24

 <210> 92
 <211> 26
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-26
 <223> Synthetic construct.

 <400> 92
 cctccagtag gtggatggat tggttc 26

 <210> 93
 <211> 47
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial sequence
 <222> 1-47
 <223> Synthetic construct.

 <400> 93
 ctcacctcat gaggatgagg ccattgtgct attcctcaac atggtag 47

 <210> 94
 <211> 3037
 <212> DNA
 <213> Homo sapiens

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 ggaigatttc atctcatta gcttctgtc tctggctatg ttggtgggat 200
 gttacgtggc cggaaatcatt ccttggctg ttaattttct agaggaacga 250
 ctctagctgg tgaactgtttt ggggtgtggc ctctctctgt gaactgctct 300
 gggagtcate gtgcctgaag gactacatgc cctttatgaa gatattcttg 350
 agggaaaaca ccaccaagca agtgaaacac ataattgtgat tgcacagac 400
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 caccagctg catgcctata ttggtgttct cctcgttctg ggttcgttt 500
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 cataaggcac cagctgcttt tggactggtt tcttcttga tgcattgctg 750
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 caccagttat gtccatggtg acatacttag gactgagtaa gacagtaaa 850
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 cgggacattt ctttatgttg ccacagtaca tgtcctcctt gaggtgggag 950
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 1550 tgg tggac catgtaagac tgggtgcttta gcatctatgc cacatgcggt
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cttcttata aatagcagat tgtagtgtca aaaaaaa 3037

<211> 95
<212> 307
<213> IRT
<213> Homo sapiens

<210> 95
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20 25 30
Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu
35 40 45
Leu Cys Gly Thr Ala Leu Ala Val Ile Val Pro Glu Gly Val His
50 55 60
Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser
65 70 75
Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser
80 85 90
Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His
95 100 105
Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu
110 115 120
Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp
125 130 135
Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu
140 145 150
Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala
155 160 165
Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val
170 175 180
Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser
185 190 195
Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His
200 205 210
Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr
215 220 225
Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

	230		235		240
Leu	Ala Thr Gly Val	Ala Met Leu Phe	Ser Ala Gly Thr	Phe Leu	
	245		250		255
Tyr	Val Ala Thr Val	His Val Leu Pro	Glu Val Gly Gly	Ile Gly	
	260		265		270
His	Ser His Lys Pro	Asp Ala Thr Gly	Gly Arg Gly Leu	Ser Arg	
	275		280		285
Leu	Glu Val Ala Ala	Leu Val Leu Gly	Cys Leu Ile Pro	Leu Ile	
	290		295		300
Leu	Ser Val Gly His	Gln His			
	305				

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 96
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<210> 97
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 97
 ctgtgctcat gtccatggac aactg 25

<210> 98
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 98
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<210> 99
 <211> 1429

<212> DNA
<213> Homo sapiens

<400> 99

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ctgattttga gatgatgggc ttgggaaacg qgcgtcgcag catgaagtcg 150
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aagcaagcag ccctggcagg gaatgacaga aacatagatg tttttaatgt 1250
tgaagatcag aaaagagaca ccataaatat acttgatcag cgtgaaaagc 1300
ggaatcatac actctgaatt gaactggaat cacatatttc acaacagggc 1350

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<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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			20						25					30

Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
			35						40					45

Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
			50						55					60

Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
			65						70					75

Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
			80						85					90

Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
			95						100					105

Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
			110						115					120

Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
			125						130					135

Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
			140						145					150

Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
			155						160					165

Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
			170						175					180

Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
			185						190					195

Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
			200						205					210

Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
			215						220					225

Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
			230						235					240

Glu	Val	Val	Leu	Asp	Ser	Lys	Arg	Gln	Val	Glu	Lys	Glu	Glu	Thr	245	250	255
Asn	Glu	Ile	Gln	Val	Val	Asn	Glu	Glu	Pro	Gln	Arg	Asp	Arg	Leu	260	265	270
Pro	Gln	Glu	Pro	Gly	Arg	Glu	Gln	Val	Val	Glu	Asp	Arg	Pro	Val	275	280	285
Gly	Gly	Arg	Gly	Phe	Gly	Gly	Ala	Gly	Glu	Leu	Gly	Gln	Thr	Pro	290	295	300
Gln	Val	Gln	Ala	Ala	Leu	Ser	Val	Ser	Gln	Glu	Asn	Pro	Glu	Met	305	310	315
Glu	Gly	Pro	Glu	Arg	Asp	Gln	Leu	Val	Ile	Pro	Asp	Gly	Gln	Glu	320	325	330
Glu	Glu	Gln	Glu	Ala	Ala	Gly	Glu	Gly	Arg	Asn	Gln	Gln	Lys	Leu	335	340	345
Arg	Gly	Glu	Asp	Asp	Tyr	Asn	Met	Asp	Glu	Asn	Glu	Ala	Glu	Ser	350	355	360
Glu	Thr	Asp	Lys	Gln	Ala	Ala	Leu	Ala	Gly	Asn	Asp	Arg	Asn	Ile	365	370	375
Asp	Val	Phe	Asn	Val	Glu	Asp	Gln	Lys	Arg	Asp	Thr	Ile	Asn	Leu	380	385	390
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 <212> DNA
 <213> Homo sapiens

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 <211> 1089
 <212> PRT
 <213> Homo sapiens

<400> 102
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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro
 35 40 45
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala
 50 55 60
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile
 65 70 75
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val
 80 85 90
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser
 95 100 105
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu
 110 115 120
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu
 125 130 135
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly
 140 145 150
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys
 155 160 165
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp
 170 175 180
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe
 185 190 195
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

	200		205		210
Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp		
	215		220		225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys		
	230		235		240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met		
	245		250		255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr		
	260		265		270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp		
	275		280		285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu		
	290		295		300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro		
	305		310		315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu		
	320		325		330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala		
	335		340		345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala		
	350		355		360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser		
	365		370		375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala		
	380		385		390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala		
	395		400		405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr		
	410		415		420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala		
	425		430		435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg		
	440		445		450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys		
	455		460		465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys		
	470		475		480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile		
	485		490		495

Ala Tyr Ala Gly	Leu	Leu	Gly	Thr	Ile	Glu	Leu	Lys	Leu	Asp	Leu	
	500					505					510	
Val Leu Leu Gly	Ala	Val	Ala	Ala	Val	Ser	Ser	Phe	Leu	Pro	Phe	
	515					520					525	
Leu Trp Lys Ala	Trp	Ala	Gly	Trp	Gly	Ser	Lys	Arg	Pro	Leu	Ala	
	530					535					540	
Thr Leu Phe Pro	Ile	Pro	Gly	Pro	Val	Leu	Leu	Leu	Leu	Leu	Phe	
	545					550					555	
Arg Leu Ala Val	Phe	Phe	Ser	Asp	Ser	Phe	Val	Val	Ala	Glu	Ala	
	560					565					570	
Arg Ala Thr Pro	Phe	Leu	Leu	Gly	Ser	Phe	Ile	Leu	Leu	Leu	Val	
	575					580					585	
Val Gln Leu His	Trp	Glu	Gly	Gln	Leu	Leu	Pro	Pro	Lys	Leu	Leu	
	590					595					600	
Thr Met Pro Arg	Leu	Gly	Thr	Ser	Ala	Thr	Thr	Asn	Pro	Pro	Arg	
	605					610					615	
His Asn Gly Ala	Tyr	Ala	Leu	Arg	Leu	Gly	Ile	Gly	Leu	Leu	Leu	
	620					625					630	
Cys Thr Arg Leu	Ala	Gly	Leu	Phe	His	Arg	Cys	Pro	Glu	Glu	Thr	
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Pro Val Cys His	Ser	Ser	Pro	Trp	Leu	Ser	Pro	Leu	Ala	Ser	Met	
	650					655					660	
Val Gly Gly Arg	Ala	Lys	Asn	Leu	Trp	Tyr	Gly	Ala	Cys	Val	Ala	
	665					670					675	
Ala Leu Val Ala	Leu	Leu	Ala	Ala	Val	Arg	Leu	Trp	Leu	Arg	Arg	
	680					685					690	
Tyr Gly Asn Leu	Lys	Ser	Pro	Glu	Pro	Pro	Met	Leu	Phe	Val	Arg	
	695					700					705	
Trp Gly Leu Pro	Leu	Met	Ala	Leu	Gly	Thr	Ala	Ala	Tyr	Trp	Ala	
	710					715					720	
Leu Ala Ser Gly	Ala	Asp	Glu	Ala	Pro	Pro	Arg	Leu	Arg	Val	Leu	
	725					730					735	
Val Ser Gly Ala	Ser	Met	Val	Leu	Pro	Arg	Ala	Val	Ala	Gly	Leu	
	740					745					750	
Ala Ala Ser Gly	Leu	Ala	Leu	Leu	Leu	Trp	Lys	Pro	Val	Thr	Val	
	755					760					765	
Leu Val Lys Ala	Gly	Ala	Gly	Ala	Pro	Arg	Thr	Arg	Thr	Val	Leu	
	770					775					780	
Thr Pro Phe Ser	Gly	Pro	Pro	Thr	Ser	Gln	Ala	Asp	Leu	Asp	Tyr	

785										790					795				
Val	Val	Pro	Gln	Ile	Tyr	Arg	His	Met	Gln	Glu	Glu	Phe	Arg	Gly					
				800					805					810					
Arg	Leu	Glu	Arg	Thr	Lys	Ser	Gln	Gly	Pro	Leu	Thr	Val	Ala	Ala					
				815					820					825					
Tyr	Gln	Leu	Gly	Ser	Val	Tyr	Ser	Ala	Ala	Met	Val	Thr	Ala	Leu					
				830					835					840					
Thr	Leu	Leu	Ala	Phe	Pro	Leu	Leu	Leu	Leu	His	Ala	Glu	Arg	Ile					
				845					850					855					
Ser	Leu	Val	Phe	Leu	Leu	Leu	Phe	Leu	Gln	Ser	Phe	Leu	Leu	Leu					
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His	Leu	Leu	Ala	Ala	Gly	Ile	Pro	Val	Thr	Thr	Pro	Gly	Pro	Phe					
				875					880					885					
Thr	Val	Pro	Trp	Gln	Ala	Val	Ser	Ala	Trp	Ala	Leu	Met	Ala	Thr					
				890					895					900					
Gln	Thr	Phe	Tyr	Ser	Thr	Gly	His	Gln	Pro	Val	Phe	Pro	Ala	Ile					
				905					910					915					
His	Trp	His	Ala	Ala	Phe	Val	Gly	Phe	Pro	Glu	Gly	His	Gly	Ser					
				920					925					930					
Cys	Thr	Trp	Leu	Pro	Ala	Leu	Leu	Val	Gly	Ala	Asn	Thr	Phe	Ala					
				935					940					945					
Ser	His	Leu	Leu	Phe	Ala	Val	Gly	Cys	Pro	Leu	Leu	Leu	Leu	Trp					
				950					955					960					
Pro	Phe	Leu	Cys	Glu	Ser	Gln	Gly	Leu	Arg	Lys	Arg	Gln	Gln	Pro					
				965					970					975					
Pro	Gly	Asn	Glu	Ala	Asp	Ala	Arg	Val	Arg	Pro	Glu	Glu	Glu	Glu					
				980					985					990					
Glu	Pro	Leu	Met	Glu	Met	Arg	Leu	Arg	Asp	Ala	Pro	Gln	His	Phe					
				995					1000					1005					
Tyr	Ala	Ala	Leu	Leu	Gln	Leu	Gly	Leu	Lys	Tyr	Leu	Phe	Ile	Leu					
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Gly	Ile	Gln	Ile	Leu	Ala	Cys	Ala	Leu	Ala	Ala	Ser	Ile	Leu	Arg					
				1025					1030					1035					
Arg	His	Leu	Met	Val	Trp	Lys	Val	Phe	Ala	Pro	Lys	Phe	Ile	Phe					
				1040					1045					1050					
Glu	Ala	Val	Gly	Phe	Ile	Val	Ser	Ser	Val	Gly	Leu	Leu	Leu	Gly					
				1055					1060					1065					
Ile	Ala	Leu	Val	Met	Arg	Val	Asp	Gly	Ala	Val	Ser	Ser	Trp	Phe					
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Arg Gln Leu Phe Leu Ala Gln Gln Arg
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<211> 1743
<212> DNA
<213> Homo sapiens

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<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
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Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
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His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
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Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
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Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Phe	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
				425					430					435	
Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<211> 21
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-21
<223> Synthetic construct

<400> 105
cgtgctgct gttgctcctg g 21

<210> 106
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 106
cagtgtgccg ggactttg 18

<210> 107
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 107
agtcgcaggc agcgttgg 18

<210> 108
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 108
ctctccgag tctgtgtgct cctgc 25

<210> 109
<211> 51
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence

<210> 1-51

thetic construct.

<211> 1114

<212> DNA

<213> 51

<210> 110

<211> 1114

<212> DNA

<213> Homo sapiens

<400> 110

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tctgtctgact gtcggcaccg cctgatgctt gcccgtagaag cccccgcag 150
gtctctgggg ggccagatc atcgggggccc acgaggtgac cccccactcc 200
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ctggggcttc gtcctgact ttgaggagct gccgcctgga ctgatggagg 600
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ctcacggcct cgttctctc tgggcctctt ggtgcggcga cccaagacc 800
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cccaggaga agccgcctga gccacaacct tgcggcatgc aaatgagatg 950
gccgtccag gcttgaatg ttcgtggct gggccccacg ggaagcctga 1000
tgttcagggt tggggtggga cgggcagcgg tggggcacac ccattccaca 1050
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..... gaaa 1114

<210> 111

<211> 283

..... PRT

<213> Homo sapiens

<400> 111

Met Gly Leu Gly Leu Arg Gly Trp Gly Arg Pro Leu Leu Thr Val
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Ala Thr Ala Leu Met Leu Pro Val Lys Pro Pro Ala Gly Ser Trp
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Gly Ala Gln Ile Ile Gly Gly His Glu Val Thr Pro His Ser Arg
35 40 45

Pro Tyr Met Ala Ser Val Arg Phe Gly Gly Gln His His Cys Gly
50 55 60

Gly Phe Leu Leu Arg Ala Arg Trp Val Val Ser Ala Ala His Cys
65 70 75

Phe Ser His Arg Asp Leu Arg Thr Gly Leu Val Val Leu Gly Ala
80 85 90

His Val Leu Ser Thr Ala Glu Pro Thr Gln Gln Val Phe Gly Ile
95 100 105

Asp Ala Leu Thr Thr His Pro Asp Tyr His Pro Met Thr His Ala
110 115 120

Asn Asp Ile Cys Leu Leu Arg Leu Asn Gly Ser Ala Val Leu Gly
125 130 135

Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
140 145 150

Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
155 160 165

Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
170 175 180

Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
185 190 195

Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
200 205 210

Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
215 220 225

Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
230 235 240

Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
245 250 255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
275 280

<210> 112

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 112

gacgtctgca acagctcctg gaag 24

<210> 113

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 113

cgaagaaggaa acgaggccgt gag 23

<210> 114

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 114

tgacacttac catgctctgc acccgccagtg gggacagcca caga 44

<210> 115

<211> 1808

<212> DNA

<213> Homo sapiens

<400> 115

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cgctgtcggc gctgggcacg gtacgaggcg ccgcctgtct gctcaaggac 150

tatgtacacg gtggggcttg ccccagcaag gccaccatcc ctgggaagac 200

250 atgtg acggggcgca acacagcat cgggaagcag accgccttgg
 300 aaaggcag gagaggaagc aacatcatcc tggcctgccg agacatggag
 350 aaagg cggcagcaaa ggacatccgc ggggaqacc ccaatcacca
 400 tgcacagcc cggcaactgg acttggcttc cctcaagtct atccagaggt
 450 ttttcaaaa gatcattgaa gaggaggagc gagtggacat tctaatcaac
 500 aatgaggggtg tgatgcgggtg cccccaactgg accaccgagg accgcttcca
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 800 actgtcaacg cctgcaccc cggcgtggcc aggacagagc tggcagaca
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 1150 aggatggcgc ctccagaccg aggacagctg tccgccatgc ccgcagcttc
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gattgcaaggt qcaagtgatca tcccgagttc aggcctctgca cggcatggag 1700
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 gctcattt 1808

<210> 116
 <211> 331
 <212> PRT
 <213> Homo sapiens

<400> 116
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 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys
 20 25 30
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly
 35 40 45
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg
 50 55 60
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys
 65 70 75
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His
 80 85 90
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg
 95 100 105
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile
 110 115 120
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr
 125 130 135
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His
 140 145 150
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala
 155 160 165
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly
 170 175 180
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn
 185 190 195
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe
 200 205 210
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117

<211> 2249

<212> DNA

<213> Homo sapiens

<400> 117

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ggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgc ctgcgcgcgc 150
agcgccggt gctggggctg ctgaggcggt acctgcgcgc ggaggaggcg 200
cggtgcggg acctgactag attctacgac aaggtacttt ctltgcctga 250
ggattcaaca acccctgtgg ctaacctct gcttgcattt actctcatca 300
aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350
gagaacatcc gagctctgaa ggatggctat gagaaggctg agcaagacct 400
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ttccgaggat cttacggaga gtggaagaca gaggatgagg caagtctaga 700

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agatgccttg galcacttgg ccttttctta ttctccggca ggaaatgttt 750
 cgtgtgacct cagcctctct cgggagtttc ttctctacac cccaaataat 800
 aagaggatgg ccaggaaatgt cttgaaatat gaaaggtctt tggcagagag 850
 cccaaccac gtggtagctg aggtgtcat ccagaagccc aatatacccc 900
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 agcccaagca gggagtgtcc cctcccaga agcatatccc agatgagtgg 2150

taattatat aaggattttt tttaaqtga aaacaacttt cttttctttt 2200

tgtatgatgg tttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

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Phe Ser Ala Leu Thr Ser Val Ala Arg Ala Leu Ala Pro Glu Arg
35 40 45

Arg Leu Leu Gly Leu Leu Arg Arg Tyr Leu Arg Gly Glu Glu Ala
50 55 60

Arg Leu Arg Asp Leu Thr Arg Phe Tyr Asp Lys Val Leu Ser Leu
65 70 75

His Glu Asp Ser Thr Thr Pro Val Ala Asn Pro Leu Leu Ala Phe
80 85 90

Thr Leu Ile Lys Arg Leu Gln Ser Asp Trp Arg Asn Val Val His
95 100 105

Ser Leu Glu Ala Ser Glu Asn Ile Arg Ala Leu Lys Asp Gly Tyr
110 115 120

Glu Lys Val Glu Gln Asp Leu Pro Ala Phe Glu Asp Leu Glu Gly
125 130 135

Ala Ala Arg Ala Leu Met Arg Leu Gln Asp Val Tyr Met Leu Asn
140 145 150

Val Lys Gly Leu Ala Arg Gly Val Phe Gln Arg Val Thr Gly Ser
155 160 165

Ala Ile Thr Asp Leu Tyr Ser Pro Lys Arg Leu Phe Ser Leu Thr
170 175 180

Gly Asp Asp Cys Phe Gln Val Gly Lys Val Ala Tyr Asp Met Gly
185 190 195

Asp Tyr Tyr His Ala Ile Pro Trp Leu Glu Glu Ala Val Ser Leu
200 205 210

Phe Arg Gly Ser Tyr Gly Glu Trp Lys Thr Glu Asp Glu Ala Ser
215 220 225

Leu Glu Asp Ala Leu Asp His Leu Ala Phe Ala Tyr Phe Arg Ala
230 235 240

Glu	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	245	250	255
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	260	265	270
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	275	280	285
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	290	295	300
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	305	310	315
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	320	325	330
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	335	340	345
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	350	355	360
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	365	370	375
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	380	385	390
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	395	400	405
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	410	415	420
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	425	430	435
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	440	445	450
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	455	460	465
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	470	475	480
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	485	490	495
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	500	505	510
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	515	520	525
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser			

Ser Pro Glu Asp

<210> 119
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 119
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<210> 120
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 120
 ggccaagtga tccaaggcat cttc 24

<210> 121
 <211> 49
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-49
 <223> Synthetic construct.

<400> 121
 ctgcgggacc tgactagatt ctacgacaag gtactttctt tgcattggg 49

<210> 122
 <211> 1778
 <212> DNA
 <213> Homo sapiens

<400> 122
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 gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150
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cggggggact cggagcaggt cggctacgc cggcgcttct cctacctctg 250
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 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcatctctct 400
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 gtgacaaact gtaccttctc caagcattca tgtacatcct tgggatctgc 500
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 gcactcctct gggcatcctg ctccccagt tctgggggt gctgctgacg 950
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050
 cgggatgctg cttgtgctac cccaattagg gccagcctg ccatggcagc 1100
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 gctgtgtgtg cctgtgtgta ggteccacgg cctctgcctc ccaggggagc 1250
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 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550
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 tcttgagcc tagttttttt ttaagtgatt ttgtaacat tcattttttt 1650

gtacagataa caggagtttc tgactaatca aagcttggtat tccccgcac 1700

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<210> 123

<211> 294

<212> PRT

<213> Homo sapiens

<400> 123

Met	Pro	Arg	Gly	Asp	Ser	Glu	Gln	Val	Arg	Tyr	Cys	Ala	Arg	Phe
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Ser	Tyr	Leu	Trp	Leu	Lys	Phe	Ser	Leu	Ile	Ile	Tyr	Ser	Thr	Val
				20					25					30

Phe	Trp	Leu	Ile	Gly	Ala	Leu	Val	Leu	Ser	Val	Gly	Ile	Tyr	Ala
				35					40					45

Glu	Val	Glu	Arg	Gln	Lys	Tyr	Lys	Thr	Leu	Glu	Ser	Ala	Phe	Leu
				50					55					60

Ala	Pro	Ala	Ile	Ile	Leu	Ile	Leu	Leu	Gly	Val	Val	Met	Phe	Met
				65					70					75

Val	Ser	Phe	Ile	Gly	Val	Leu	Ala	Ser	Leu	Arg	Asp	Asn	Leu	Tyr
				80					85					90

Leu	Leu	Gln	Ala	Phe	Met	Tyr	Ile	Leu	Gly	Ile	Cys	Leu	Ile	Met
				95					100					105

Glu	Leu	Ile	Gly	Gly	Val	Val	Ala	Leu	Thr	Phe	Arg	Asn	Gln	Thr
				110					115					120

Ile	Asp	Phe	Leu	Asn	Asp	Asn	Ile	Arg	Arg	Gly	Ile	Glu	Asn	Tyr
				125					130					135

Tyr	Asp	Asp	Leu	Asp	Phe	Lys	Asn	Ile	Met	Asp	Phe	Val	Gln	Lys
				140					145					150

Lys	Phe	Lys	Cys	Cys	Gly	Gly	Glu	Asp	Tyr	Arg	Asp	Trp	Ser	Lys
				155					160					165

Asn	Gln	Tyr	His	Asp	Cys	Ser	Ala	Pro	Gly	Pro	Leu	Ala	Cys	Gly
				170					175					180

Val	Pro	Tyr	Thr	Cys	Cys	Ile	Arg	Asn	Thr	Thr	Glu	Val	Val	Asn
				185					190					195

Thr	Met	Cys	Gly	Tyr	Lys	Thr	Ile	Asp	Lys	Glu	Arg	Phe	Ser	Val
				200					205					210

Gln	Asp	Val	Ile	Tyr	Val	Arg	Gly	Cys	Thr	Asn	Ala	Val	Ile	Ile
				215					220					225

Trp	Phe	Met	Asp	Asn	Tyr	Thr	Ile	Met	Ala	Cys	Ile	Leu	Leu	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 124
 atcatctatt ccacccgtgtt ctggc 25

<210> 125
 <211> 25
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

<400> 125
 gacagagtgc tccatgatga tgtcc 25

<210> 126
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 126
 cctgtctgtg ggcatttatg cagaggttga gcggcagaaa tataaaaccc 50

<210> 127
 <211> 1636
 <212> DNA
 <213> Homo sapiens

<450> 127

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ctctgtggtt tgcctggcagc caccttgatc caagccaccc tcagtccac 150
tgcagttctc atctctggcc caaaagtcac caaagaaaag ctgacacagg 200
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gaccatcgtg gagtccaca tgacgactga ggcccaagcc accatccgca 500
tggacaccag tgcaagtgc cccaccgcc tggctctcag tgactgtgc 550
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ggtgaacgcc ttagctaagc aggtcatgaa cctctagtg ccatccctgc 650
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ggcatgtatg cagacctct gcagctggtg aaggtgccca ttctctcag 750
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<210> 128
 <211> 484
 <212> PRT
 <213> Homo sapiens

<400> 128
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 35 40 45
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser
 50 55 60
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser
 65 70 75
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile
 80 85 90
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp
 95 100 105
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe
 110 115 120
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr
 125 130 135
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro
 140 145 150
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu
 155 160 165
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu
 170 175 180
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu
 185 190 195
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly
 200 205 210
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu
 215 220 225

Leu	Asp	Arg	Leu	Glu	Phe	Asp	Leu	Leu	Tyr	Pro	Ala	Ile	Lys
			230					235					240
Gln	Asp	Thr	Ile	Gln	Leu	Tyr	Leu	Gly	Ala	Lys	Leu	Leu	Asp
			245					250					255
Gln	Gly	Lys	Val	Thr	Lys	Trp	Phe	Asn	Asn	Ser	Ala	Ala	Ser
			260					265					270
Thr	Met	Pro	Thr	Leu	Asp	Asn	Ile	Pro	Phe	Ser	Leu	Ile	Val
			275					280					285
Gln	Asp	Val	Val	Lys	Ala	Ala	Val	Ala	Ala	Val	Leu	Ser	Pro
			290					295					300
Glu	Phe	Met	Val	Leu	Leu	Asp	Ser	Val	Leu	Pro	Glu	Ser	Ala
			305					310					315
Arg	Leu	Lys	Ser	Ser	Ile	Gly	Leu	Ile	Asn	Glu	Lys	Ala	Ala
			320					325					330
Lys	Leu	Gly	Ser	Thr	Gln	Ile	Val	Lys	Ile	Leu	Thr	Gln	Asp
			335					340					345
Pro	Glu	Phe	Phe	Ile	Asp	Gln	Gly	His	Ala	Lys	Val	Ala	Gln
			350					355					360
Ile	Val	Leu	Glu	Val	Phe	Pro	Ser	Ser	Glu	Ala	Leu	Arg	Pro
			365					370					375
Phe	Thr	Leu	Gly	Ile	Glu	Ala	Ser	Ser	Glu	Ala	Gln	Phe	Tyr
			380					385					390
Lys	Gly	Asp	Gln	Leu	Ile	Leu	Asn	Leu	Asn	Asn	Ile	Ser	Ser
			395					400					405
Arg	Ile	Gln	Leu	Met	Asn	Ser	Gly	Ile	Gly	Trp	Phe	Gln	Pro
			410					415					420
Val	Leu	Lys	Asn	Ile	Ile	Thr	Glu	Ile	Ile	His	Ser	Ile	Leu
			425					430					435
Pro	Asn	Gln	Asn	Gly	Lys	Leu	Arg	Ser	Gly	Val	Pro	Val	Ser
			440					445					450
Val	Lys	Ala	Leu	Gly	Phe	Glu	Ala	Ala	Glu	Ser	Ser	Leu	Thr
			455					460					465
Asp	Ala	Leu	Val	Leu	Thr	Pro	Ala	Ser	Leu	Trp	Lys	Pro	Ser
			470					475					480

Pro Val Ser Gln

<210> 129
 <211> 2213
 <212> DNA
 <213> Homo sapiens

129

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 aaaaaaaaaa aaa 2213

<210> 130
 <211> 335
 <212> PRT
 <213> Homo sapiens

<400> 130
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 20 25 30
 Arg Lys Lys Glu Met Val Leu Ser Glu Lys Val Ser Gln Leu Met
 35 40 45
 Glu Trp Thr Asn Lys Arg Pro Val Ile Arg Met Asn Gly Asp Lys
 50 55 60
 Phe Arg Arg Leu Val Lys Ala Pro Pro Arg Asn Tyr Ser Val Ile
 65 70 75
 Val Met Phe Thr Ala Leu Gln Leu His Arg Gln Cys Val Val Cys
 80 85 90
 Lys Gln Ala Asp Glu Glu Phe Gln Ile Leu Ala Asn Ser Trp Arg
 95 100 105

Tyr	Ser	Ser	Ala	Phe	Thr	Asn	Arg	Ile	Phe	Phe	Ala	Met	Val	Asp	
				110					115					120	
Phe	Asp	Glu	Gly	Ser	Asp	Val	Phe	Gln	Met	Leu	Asn	Met	Asn	Ser	
				125					130					135	
Ala	Pro	Thr	Phe	Ile	Asn	Phe	Pro	Ala	Lys	Gly	Lys	Pro	Lys	Arg	
				140					145					150	
Gly	Asp	Thr	Tyr	Glu	Leu	Gln	Val	Arg	Gly	Phe	Ser	Ala	Glu	Gln	
				155					160					165	
Ile	Ala	Arg	Trp	Ile	Ala	Asp	Arg	Thr	Asp	Val	Asn	Ile	Arg	Val	
				170					175					180	
Ile	Arg	Pro	Pro	Asn	Tyr	Ala	Gly	Pro	Leu	Met	Leu	Gly	Leu	Leu	
				185					190					195	
Leu	Ala	Val	Ile	Gly	Gly	Leu	Val	Tyr	Leu	Arg	Arg	Ser	Asn	Met	
				200					205					210	
Glu	Phe	Leu	Phe	Asn	Lys	Thr	Gly	Trp	Ala	Phe	Ala	Ala	Leu	Cys	
				215					220					225	
Phe	Val	Leu	Ala	Met	Thr	Ser	Gly	Gln	Met	Trp	Asn	His	Ile	Arg	
				230					235					240	
Gly	Pro	Pro	Tyr	Ala	His	Lys	Asn	Pro	His	Thr	Gly	His	Val	Asn	
				245					250					255	
Tyr	Ile	His	Gly	Ser	Ser	Gln	Ala	Gln	Phe	Val	Ala	Glu	Thr	His	
				260					265					270	
Ile	Val	Leu	Leu	Phe	Asn	Gly	Gly	Val	Thr	Leu	Gly	Met	Val	Leu	
				275					280					285	
Leu	Cys	Glu	Ala	Ala	Thr	Ser	Asp	Met	Asp	Ile	Gly	Lys	Arg	Lys	
				290					295					300	
Ile	Met	Cys	Val	Ala	Gly	Ile	Gly	Leu	Val	Val	Leu	Phe	Phe	Ser	
				305					310					315	
Trp	Met	Leu	Ser	Ile	Phe	Arg	Ser	Lys	Tyr	His	Gly	Tyr	Pro	Tyr	
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Ser	Phe	Leu	Met	Ser											
				335											

<210> 131
 <211> 2476
 <212> DNA
 <213> Homo sapiens

<400> 131
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 ggcnaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250
 ggttaacat ttcatccagg aagtcaggta gtgaaactc cttttatcaa 300
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 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550
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 taatcttact cgtaacagga ctaaagtcag agtgatggaa agggattggc 650
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ctccgtccaccagttataat aaagagcagc ttatcaagtg gaaacaaagt 1600
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<210> 132
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 132
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 20 25 30
 Ala Pro Asn Val Val Leu Val Val Ser Asp Ser Phe Asp Gly Arg
 35 40 45
 Leu Thr Phe His Pro Gly Ser Gln Val Val Lys Leu Pro Phe Ile
 50 55 60
 Asn Phe Met Lys Thr Arg Gly Thr Ser Phe Leu Asn Ala Tyr Thr
 65 70 75

Asn	Pro	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Lys	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	

365	370	375
Leu Ser Gly Tyr Ser Leu Leu Pro Leu Ser Ser Glu Thr Phe Lys		
380	385	390
Asn Glu His Lys Val Lys Asn Leu His Pro Pro Trp Ile Leu Ser		
395	400	405
Glu Phe His Gly Cys Asn Val Asn Ala Ser Thr Tyr Met Leu Arg		
410	415	420
Thr Asn His Trp Lys Tyr Ile Ala Tyr Ser Asp Gly Ala Ser Ile		
425	430	435
Leu Pro Gln Leu Phe Asp Leu Ser Ser Asp Pro Asp Glu Leu Thr		
440	445	450
Asn Val Ala Val Lys Phe Pro Glu Ile Thr Tyr Ser Leu Asp Gln		
455	460	465
Lys Leu His Ser Ile Ile Asn Tyr Pro Lys Val Ser Ala Ser Val		
470	475	480
His Gln Tyr Asn Lys Glu Gln Phe Ile Lys Trp Lys Gln Ser Ile		
485	490	495
Gly Gln Asn Tyr Ser Asn Val Ile Ala Asn Leu Arg Trp His Gln		
500	505	510
Asp Trp Gln Lys Glu Pro Arg Lys Tyr Glu Asn Ala Ile Asp Gln		
515	520	525
Trp Leu Lys Thr His Met Asn Pro Arg Ala Val		
530	535	

<210> 133
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 133
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 ctacatccta ggccttctgg ggcctttggg cacactgggt gccatgctgc 200
 tccccagctg gaaaacaagt tcttatgtcg gtgccagcat tgtgacagca 250
 gttggcttct ccaagggcct ctggatggaa tgtgccacac acagcacagg 300
 catcaccag tgtgacatct atagcaccct tctgggcctg cccgtgaca 350
 tccaggctgc ccaggccatg atggtgacat ccagtgaat ctctccctg 400
 gcttgcattt tctctgtggg ggcatgaga tgcacagctt tctgccagga 450

ctccagagct ctgagacagag tggcgatagc aggtggagtc ttttccatcc 500
 ttggagagct cctgggattc attcctgttg cctggaatct tcatgggata 550
 ctacgggaact tctactcacc actgggtgct gacagcatga aatttgagat 600
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 ctggaatcat cctctgcttt tctgtctcat cccagagaaa tgcctccaac 700
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<210> 134

<211> 230

<212> PRT

<213> Homo sapiens

<400> 134

Met	Ala	Ser	Leu	Gly	Leu	Gln	Leu	Val	Gly	Tyr	Ile	Leu	Gly	Leu
1				5					10					15

Leu	Gly	Leu	Leu	Gly	Thr	Leu	Val	Ala	Met	Leu	Leu	Pro	Ser	Trp
				20					25					30

Lys	Thr	Ser	Ser	Tyr	Val	Gly	Ala	Ser	Ile	Val	Thr	Ala	Val	Gly
				35					40					45

Phe	Ser	Lys	Gly	Leu	Trp	Met	Glu	Cys	Ala	Thr	His	Ser	Thr	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	30		45		60
Ile Thr Gln Cys Asp Ile Tyr Ser Thr	65	Leu Leu Gly Leu Pro Ala	70		75
Asp Ile Gln Ala Ala Gln Ala Met Met	80	Val Thr Ser Ser Ala Ile	85		90
Ser Ser Leu Ala Cys Ile Ile Ser Val	95	Val Gly Met Arg Cys Thr	100		105
Val Phe Cys Gln Glu Ser Arg Ala Lys	110	Asp Arg Val Ala Val Ala	115		120
Gly Gly Val Phe Phe Ile Leu Gly Gly	125	Leu Leu Gly Phe Ile Pro	130		135
Val Ala Trp Asn Leu His Gly Ile Leu	140	Arg Asp Phe Tyr Ser Pro	145		150
Leu Val Pro Asp Ser Met Lys Phe Glu	155	Ile Gly Glu Ala Leu Tyr	160		165
Leu Gly Ile Ile Ser Ser Leu Phe Ser	170	Leu Ile Ala Gly Ile Ile	175		180
Leu Cys Phe Ser Cys Ser Ser Gln Arg	185	Asn Arg Ser Asn Tyr Tyr	190		195
Asp Ala Tyr Gln Ala Gln Pro Leu Ala	200	Thr Arg Ser Ser Pro Arg	205		210
Pro Gly Gln Pro Pro Lys Val Lys Ser	215	Glu Phe Asn Ser Tyr Ser	220		225
Leu Thr Gly Tyr Val	230				

<210> 135

<211> 610

<212> DNA

<213> Homo sapiens

<400> 135

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aagtcacggc tcccgtctggc tcagaaccat ggctgtgcca gccggcaccc 150
agggtgtggag acaagatcta caaccctctg gaggcagtgt gttacaatga 200
cgccatcgtg tccctgagcg agaccggcca atgtgggtccc cctgcacct 250
tctggccctg ctttgagctc tctgtctctg attcctttgg cctcacaac 300
gattttgttg tgaagctgaa ggttcagggt gtgaattccc agtgcacac 350

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atctcccatc tccagtaaat gtgaaacacg aagacgtttt cccagagaag 400
 acatagaag aaaatcaact ttcactaagg catctcagaa acataaggeta 450
 aggtaatatg tgtaccagta gagaagccctg aggaattttac aaaatgatgc 500
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550
 atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600
 acctgtaaaa 610

<210> 136
 <211> 119
 <212> PRT
 <213> Homo sapiens

<400> 136
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu
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 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu
 20 25 30
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr
 35 40 45
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu
 50 55 60
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys
 65 70 75
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe
 80 85 90
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser
 95 100 105
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro
 110 115

<210> 137
 <211> 771
 <212> DNA
 <213> Homo sapiens

<400> 137
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 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200
 gtctgtccct tggccaggac ccagacgtgt ggaactgca ccttcagagt 250

ctgtttgag cagtgtgtg cctggacatt catggtgaa ctgataaacc 300
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 tgggctctga gaaagagggc ggtgttaact gagatctggg atgctgagtg 450
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<210> 138

<211> 110

<212> PRT

<213> Homo sapiens

<400> 138

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Ile	Ser	Arg	Leu	Leu	Cys	Ser	His	Gly	Ala	Pro	Val	Ala	Pro	Met	20	25	30	
Thr	Pro	Tyr	Leu	Met	Leu	Cys	Gln	Pro	His	Lys	Arg	Cys	Gly	Asp	35	40	45	
Lys	Phe	Tyr	Asp	Pro	Leu	Gln	His	Cys	Cys	Tyr	Asp	Asp	Ala	Val	50	55	60	
Val	Pro	Leu	Ala	Arg	Thr	Gln	Thr	Cys	Gly	Asn	Cys	Thr	Phe	Arg	65	70	75	
Val	Cys	Phe	Glu	Gln	Cys	Cys	Pro	Trp	Thr	Phe	Met	Val	Lys	Leu	80	85	90	
Ile	Asn	Gln	Asn	Cys	Asp	Ser	Ala	Arg	Thr	Ser	Asp	Asp	Arg	Leu	95	100	105	
Cys	Arg	Ser	Val	Ser	110													

<210> 139

<211> 2044

<212> DNA

<213> Homo sapiens

<400> 139

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 400 tctggccc tggaggccg cagctgggc tggggtccc tctcttgc 200
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 900 ggcctatccg caacctcag ttccaggacc ttccctgca ccatggagge 450
 1000 caccaggctg ccaacaccag ccacgacctg gctcagcgc accggctgga 500
 1100 gtggcctcc gaccacctg gcaacttctc catcaccatg cgcacctga 550
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 1300 caccactcg agcacagggt ccatggtgcc atggagctgc aggtgcagac 650
 1400 aggcaaagat gcaccatcca actgtgtggt gtaccatcc tctcccagg 700
 1500 atagtgaata catcacggtt gcagccctgg ctacgggtgc ctgcctgta 750
 1600 ggaatcctc gctccccct catcctgtct ctggtctaca agcaaaggca 800
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 1900 ataccgagg ccaaagtcag gcacccctg tctatgtgg ccagcgcca 950
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 2200 gactctcaa actttgaggt catctagccc agctggggga cagtgggctg 1100
 2300 ttgtggtgg gtctggggca ggtgcatttg agccagggtt ggtctgtga 1150
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 2700 agattctccc ctagagacct gaaattcacc agctacagat gccaatgac 1350
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 2900 tgagacatga gcttgggat gtggcagcat cagtgggaca agatggacac 1450

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 ctccactgc tcagcgggg ccattgcaag ggtgcacac aatgtcttct 1950
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 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140
 <211> 311
 <212> PRT
 <213> Homo sapiens

<400> 140
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 Ala Ala Phe Lys Val Ala Thr Pro Tyr Ser Leu Tyr Val Cys Pro
 35 40 45
 Glu Gly Gln Asn Val Thr Leu Thr Cys Arg Leu Leu Gly Pro Val
 50 55 60
 Asp Lys Gly His Asp Val Thr Phe Tyr Lys Thr Trp Tyr Arg Ser
 65 70 75
 Ser Arg Gly Glu Val Gln Thr Cys Ser Glu Arg Arg Pro Ile Arg
 80 85 90
 Asn Leu Thr Phe Gln Asp Leu His Leu His His Gly Gly His Gln
 95 100 105
 Ala Ala Asn Thr Ser His Asp Leu Ala Gln Arg His Gly Leu Glu
 110 115 120
 Ser Ala Ser Asp His His Gly Asn Phe Ser Ile Thr Met Arg Asn
 125 130 135
 Leu Thr Leu Leu Asp Ser Gly Leu Tyr Cys Cys Leu Val Val Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141

<211> 1732

<212> DNA

<213> Homo sapiens

<400> 141

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<210> 142
<211> 451
<212> PRT
<213> Homo sapiens
<400> 142

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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

	290		295		300
Arg His Pro Glu	Lys Val Ala Gly Lys	Cys Cys Lys Ile Cys	Pro		
	305		310		315
Glu Asp Lys Ala	Asp Pro Gly His Ser	Glu Ile Ser Ser Thr	Arg		
	320		325		330
Cys Pro Lys Ala	Pro Gly Arg Val Leu	Val His Thr Ser Val	Ser		
	335		340		345
Pro Ser Pro Asp	Asn Leu Arg Arg Phe	Ala Leu Glu His Glu	Ala		
	350		355		360
Ser Asp Leu Val	Glu Ile Tyr Leu Trp	Lys Leu Val Lys Asp	Glu		
	365		370		375
Glu Thr Glu Ala	Gln Arg Gly Glu Val	Pro Gly Pro Arg Pro	His		
	380		385		390
Ser Gln Asn Leu	Pro Leu Asp Ser Asp	Gln Glu Ser Gln Glu	Ala		
	395		400		405
Arg Leu Pro Glu	Arg Gly Thr Ala Leu	Pro Thr Ala Arg Trp	Pro		
	410		415		420
Pro Arg Arg Ser	Leu Glu Arg Leu Pro	Ser Pro Asp Pro Gly	Ala		
	425		430		435
Glu Gly His Gly	Gln Ser Arg Gln Ser	Asp Gln Asp Ile Thr	Lys		
	440		445		450

Thr

<210> 143
 <211> 693
 <212> DNA
 <213> Homo sapiens

<400> 143
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150
 tgggctacgc gctctcggtt atcgtgaccc cgggagagcg gcggaagcag 200
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300
 cgcaggagaa cgtggcctgg aggaagaact ggatggttg cggcgaaggc 350
 ggcgcagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccc 400
 gaccttggct tgggcgcagg aatccgaggg agcctttctc cttegtgggc 450

cctccgaga gtcgggaccg agataccatg ccaggactct ccgggggtct 500
 gtcagctgcc gtcgggtgag cactgttccc ccaaaccctg gaactgaatgc 550
 ttcctgctc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600
 cctgaaaga accaataaaa tcatgttctt ccaaaaaaaaaa aaaaaaaaaa 650
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144
 <211> 93
 <212> PRT
 <213> Homo sapiens

<400> 144
 Met Asp Ser Leu Arg Lys Met Leu Ile Ser Val Ala Met Leu Gly
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 Ala Gly Ala Gly Val Gly Tyr Ala Leu Leu Val Ile Val Thr Pro
 20 25 30
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln
 35 40 45
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu
 50 55 60
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala
 65 70 75
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly
 80 85 90
 Arg Ser Pro

<210> 145
 <211> 1883
 <212> DNA
 <213> Homo sapiens

<400> 145
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 ttgaggggaa gaggctgact gtacgttctt tctactctgg caccactctc 100
 caggtgccca tggggcccag caccctcttc ctcatcttgt tctttttgtc 150
 atggtcggga ccctccaag gacagcagca ccaccttgtg gactacatgg 200
 aacgccgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250
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 29. ...gaanatcac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850

aaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146
<211> 406
<212> FRT
<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147
 <211> 2052
 <212> DNA
 <213> Homo sapiens

<400> 147
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 ccgctcacgc agagcctctc cgtggcttcc qcaccttgag cattaggcca 100
 gttctcctct tctctctaatt ccattccgtca cctctcctgt catccgtttc 150
 catgccgtga ggtccattca cagaacacat ccattggctct catgctcagt 200
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtggttgg 250
 gccagacaag cctgtccagg ccttgggtggg ggaggacgca gcattctcct 300
 gtttctgttc tcttaagacc aatgcagagg ccattggaagt gcggttcttc 350
 agggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450
 attctattgc ggaggggcgc atctctctga ggetggaaaa cattactgtg 500

ttggtgctg geetctatgg gtgcaggatt adtccccagt cttactacca 550
 gaagggcctac tgggagctac aggtgtcagc actgggctca gttcctctca 600
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtc 650
 tggggtggt tccccgggc cacagogaag tggaaaggtc cacaaggaca 700
 gatttgttc acagactcca ggacaaacag agacatgcat ggctgtttg 750
 atgtggagat ctctctgacc gtccaagaga acgcccggag catatcctgt 800
 tccatgggc atgtcatct gagccgagag gtggaatcca gggtaacagat 850
 aggagatacc tttttcgagc ctatctgtg gcacctggt accaaagtac 900
 tgggaatact ctgtgtggc ctattttttg gcattgttg actgaagatt 950
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 aaaqcacga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050
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 aacattactg ggaggtggac ggaggacaca ataaaagggtg gcgcgtggga 1250
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 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350
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 ataggggtct tctggacta tgagtgtggg accatctct tcttcaacat 1450
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 aagggcctct gcaatcccag agacaagcaa cagtgagtc tctcacagg 1650
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 ccacctctca ggtgaagaac cgtcaggaat tccatctca caggctgtgg 1950

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acgactgata tctaatgggt ttgttcattt tattacactt tcagtaaaaa 2050

11 52

<210> 148

<211> 500

<212> PRT

<213> Homo sapiens

<400> 148

Met Ala Leu Met Leu Ser Leu Val Leu Ser Leu Leu Lys Leu Gly
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Ser Gly Gln Trp Gln Val Phe Gly Pro Asp Lys Pro Val Gln Ala
20 25 30

Leu Val Gly Glu Asp Ala Ala Phe Ser Cys Phe Leu Ser Pro Lys
35 40 45

Thr Asn Ala Glu Ala Met Glu Val Arg Phe Phe Arg Gly Gln Phe
50 55 60

Ser Ser Val Val His Leu Tyr Arg Asp Gly Lys Asp Gln Pro Phe
65 70 75

Met Gln Met Pro Gln Tyr Gln Gly Arg Thr Lys Leu Val Lys Asp
80 85 90

Ser Ile Ala Glu Gly Arg Ile Ser Leu Arg Leu Glu Asn Ile Thr
95 100 105

Val Leu Asp Ala Gly Leu Tyr Gly Cys Arg Ile Ser Ser Gln Ser
110 115 120

Tyr Tyr Gln Lys Ala Ile Trp Glu Leu Gln Val Ser Ala Leu Gly
125 130 135

Ser Val Pro Leu Ile Ser Ile Thr Gly Tyr Val Asp Arg Asp Ile
140 145 150

Gln Leu Leu Cys Gln Ser Ser Gly Trp Phe Pro Arg Pro Thr Ala
155 160 165

Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Thr Asp Ser Arg
170 175 180

Thr Asn Arg Asp Met His Gly Leu Phe Asp Val Glu Ile Ser Leu
185 190 195

Thr Val Gln Glu Asn Ala Gly Ser Ile Ser Cys Ser Met Arg His
200 205 210

Ala His Leu Ser Arg Glu Val Glu Ser Arg Val Gln Ile Gly Asp
215 220 225

Thr Phe Phe Glu Pro Ile Ser Trp His Leu Ala Thr Lys Val Leu

	230		235		240
Leu Cys Cys Gly Leu Phe Phe	245	Gly Ile Val Gly Leu Lys	255		
Ile Phe Phe Ser Lys Phe Gln Trp Lys	260	Ile Gln Ala Glu Leu Asp	270		
Arg Arg Arg Lys His Gly Gln Ala Glu	275	Leu Arg Asp Ala Arg Lys	285		
His Ala Val Glu Val Thr Leu Asp Pro	290	Glu Thr Ala His Pro Lys	300		
Leu Cys Val Ser Asp Leu Lys Thr Val	305	Thr His Arg Lys Ala Pro	315		
Gln Glu Val Pro His Ser Glu Lys Arg	320	Phe Thr Arg Lys Ser Val	330		
Val Ala Ser Gln Ser Phe Gln Ala Gly	335	Lys His Tyr Trp Glu Val	345		
Asp Gly Gly His Asn Lys Arg Trp Arg	350	Val Gly Val Cys Arg Asp	360		
Asp Val Asp Arg Arg Lys Glu Tyr Val	365	Thr Leu Ser Pro Asp His	375		
Gly Tyr Trp Val Leu Arg Leu Asn Gly	380	Glu His Leu Tyr Phe Thr	390		
Leu Asn Pro Arg Phe Ile Ser Val Phe	395	Pro Arg Thr Pro Pro Thr	405		
Lys Ile Gly Val Phe Leu Asp Tyr Glu	410	Cys Gly Thr Ile Ser Phe	420		
Phe Asn Ile Asn Asp Gln Ser Leu Ile	425	Tyr Thr Leu Thr Cys Arg	435		
Phe Glu Gly Leu Leu Arg Pro Tyr Ile	440	Glu Tyr Pro Ser Tyr Asn	450		
Glu Gln Asn Gly Thr Pro Ile Val Ile	455	Cys Pro Val Thr Gln Glu	465		
Ser Glu Lys Glu Ala Ser Trp Gln Arg	470	Ala Ser Ala Ile Pro Glu	480		
Thr Ser Asn Ser Glu Ser Ser Ser Gln	485	Ala Thr Thr Pro Phe Leu	495		
Pro Arg Gly Glu Met	500				

<210> 149

<211> 24

<210> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 149
gggtgggtcca cctctacagg gacg 24

<210> 150
<211> 23
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-23
<223> Synthetic construct.

<400> 150
ggaactgacc cagtgcctgac acc 23

<210> 151
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 151
gcagatgcc aagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152
<211> 2294
<212> DNA
<213> Homo sapiens

<400> 152
gcatgtgtgc gcccggtggc ggtggcgggc gcggttgccg aggettectt 50
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctgggcg 150
gcctcgcctt gttgtgctgc gccgcgcgcg ccgcgcgcgt cgcctcagcc 200
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 atgttatatt taatgtcagg atttaaaaa acataattta ctgatttagt 1100
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 ctgggttgtt ttaatttcaa aagaaatatta tggactgaaa tgagagaaca 1850

tctttaaaga acattttagct ccttgacaaa gaagtgcctt atactttagc 1900
 actaaatatt ttaaatgctt tataaatgat attataactgt tatggaatat 1950
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 ctcacgcctg taatactaga acttiggag gccaggcgg gtgatacaat 2050
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 ctactaaaaa tacaacaaa ttagctgggc gtgggtggcc acacctgtag 2150
 tcccagctac tcgggagget gaggcaggag aatcggttga acccgggagg 2200
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 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153

<211> 258

<212> PRT

<213> Homo sapiens

<400> 153

Met	Arg	Ser	Leu	Pro	Ser	Leu	Gly	Gly	Leu	Ala	Leu	Leu	Cys	Cys	
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Ala	Ala	Ala	Ala	Ala	Ala	Val	Ala	Ser	Ala	Ala	Ser	Ala	Gly	Asn	
				20					25					30	
Val	Thr	Gly	Gly	Gly	Gly	Ala	Ala	Gly	Gln	Val	Asp	Ala	Ser	Pro	
				35					40					45	
Gly	Pro	Gly	Leu	Arg	Gly	Glu	Pro	Ser	His	Pro	Phe	Pro	Arg	Ala	
				50					55					60	
Thr	Ala	Pro	Thr	Ala	Gln	Ala	Pro	Arg	Thr	Gly	Pro	Pro	Arg	Ala	
				65					70					75	
Thr	Val	His	Arg	Pro	Leu	Ala	Ala	Thr	Ser	Pro	Ala	Gln	Ser	Pro	
				80					85					90	
Glu	Thr	Thr	Pro	Leu	Trp	Ala	Thr	Ala	Gly	Pro	Ser	Ser	Thr	Thr	
				95					100					105	
Phe	Gln	Ala	Pro	Leu	Gly	Pro	Ser	Pro	Thr	Thr	Pro	Pro	Ala	Ala	
				110					115					120	
Glu	Arg	Thr	Ser	Thr	Thr	Ser	Gln	Ala	Pro	Thr	Arg	Pro	Ala	Pro	
				125					130					135	
Thr	Thr	Leu	Ser	Thr	Thr	Thr	Gly	Pro	Ala	Pro	Thr	Thr	Pro	Val	
				140					145					150	
Ala	Thr	Thr	Val	Pro	Ala	Pro	Thr	Thr	Pro	Arg	Thr	Pro	Thr	Pro	
				155					160					165	
Asp	Leu	Pro	Ser	Ser	Ser	Asn	Ser	Ser	Val	Leu	Pro	Thr	Pro	Pro	

	170	175	180
Arg Thr Glu Ala Pro Ser Ser Pro Pro Pro Glu Tyr Val Cys Asn			
	185	190	195
Cys Ser Val Val Gly Ser Leu Asn Val Asn Arg Cys Asn Gln Thr			
	200	205	210
Thr Gly Gln Cys Glu Cys Arg Pro Gly Tyr Gln Gly Leu His Cys			
	215	220	225
Glu Thr Cys Lys Glu Gly Phe Tyr Leu Asn Tyr Thr Ser Gly Leu			
	230	235	240
Cys Gln Pro Cys Asp Cys Ser Pro His Gly Ala Leu Ser Ile Pro			
	245	250	255

Cys Asn Arg

<210> 154
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 154
 aactgctctg tggttggaag cctg 24

<210> 155
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 155
 cagtcacatg gctgacagac ccac 24

<210> 156
 <211> 38
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-38
 <223> Synthetic construct.

<400> 156
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157
 <211> 689
 <212> DNA
 <213> Homo sapiens

<400> 157
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 ctggaccctg agcagcttct tgggcctgg tacgtgcttg cggtggcctc 150
 cgggaaaaag ggtttgcca tggagaagga catgaagaac gtcgtggggg 200
 tgggtggtac cctcactcca gaaaacaacc tgcggacgt gtcctctcag 250
 caggggctgg gagggtgtga ccagagtgtc atggacctga taaagcgaan 300
 ctccggatgg gtgtttgaga atccctcaat aggcctgtg gagctctggg 350
 tgctggccac caacttcaga gactatgcca tcatcttacc tcagctggag 400
 ttccggggac agcccttcaa caccgtggag ctgtacagtc tgacggagac 450
 agccagccag gaggccatgg ggctcttcac caagtggagg aggagcctgg 500
 gcttctgtc acagtagcag gccagctgc agaaggacct cactgtgt 550
 cacaagatcc ttctgtgagt gctgcgtccc cagtagggat ggcgccaca 600
 gggctctgt acctcggcca gtgtccacc acctcgtcca ggcgtcccc 650
 gggccagca ccagctcaga ataaagcgt tccacagca 689

<210> 158
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 158
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val
 1 5 10 15
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln
 20 25 30
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys
 35 40 45
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val
 50 55 60
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln
 65 70 75
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys
 80 85 90

Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95					100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile
			110						115				120
Leu	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val
			125						130				135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly
			140						145				150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln	
			155						160				

<210> 159

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 159

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gtaaactgct gacgatgcag agtaccgtga cggcgcagga aggcctgtgt 150
gtccatgtgc cctgctcctt ctccacccc tcgcattggt ggatttaccc 200
tgccccagta gttcatgggt actgggttcg ggaagggggc aatacagacc 250
aggatgctcc agtggccaca aacaacccag ctccgggcagt gtgggaaggag 300
actcgggacc gattccacct ccttggggac ccacatacca agaattgcac 350
cctgagcatt agagatgcca gaagaagtga tgcggggaga tacttcttct 400
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gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500
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gccccaggac catggcacca gctcaccctg tcaggtgacc ttccctgggg 700
ccagcgtgac cagcaacaag accgtccatc tcaacgtgtc ctaccgcct 750
cagaacttga ccatgactgt ctccaagga gacggcacag tatccacagt 800
cttgggaaat ggctcatctc tgtcactccc agagggccag tctctgogcc 850
tggtctgtgc agttgatgca gttgacagca atccccctgc caggetgagc 900
ctgagcttga gaggcctgac cctgtgcccc tcacagcctt caaacccggg 950

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ggt ttgag ctgccttggg tgcacctgag ggaatgcagct gaattcacct 1000
 gaa ggcctca gaacctcttc ggccttcagg aggtctacct gaacgtctcc 1050
 ttt taaaca aagccacatc aggagtgact cagggggtgg tggggggagg 1100
 ttgagccaca gccctgggtct tccigtccct ctgcgtcacc ttcgttgtag 1150
 ttgggtcctg caggaagaaa tgggcaaggc cagcagcggg cttggggagat 1200
 acgggcctag aggatgcaaa cgtgttcagg ggttcagcct ctcaggggccc 1250
 cttgactgaa ccttggggcag aagacagctc cccagaccag cctccccag 1300
 cttctgcccg ctcttcagtg ggggaaggag agctccagta tgcateccctc 1350
 agttccaga tggatgaagcc ttgggaactcg cggggacagg aggcactga 1400
 caccagctac tgggagatca agatccacag atgagaaact gcagagactc 1450
 acctgattg agggatcaca gcccctccag gcaagggaga agtcagaggc 1500
 tgattcttgt agaattaaca gcccctcaag tgatgagcta tgataaacct 1550
 atgaattatg tgcagagtga aaagcacaca ggccttagag tcaaagtatc 1600
 tcaaacctga atccacactg tgcctccct tttatttttt taactaaaag 1650
 acagacaaat tccca 1665

<210> 160
 <211> 463
 <212> PRT
 <213> Homo sapiens

<400> 160
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 1 5 10 15
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr
 20 25 30
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr
 35 40 45
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr
 50 55 60
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala
 65 70 75
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg
 80 85 90
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser
 95 100 105
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu	110	115	120
	125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile	140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser	155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp	170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser	185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser	200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn	215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr	230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly	245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu	260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu	275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser	290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala	305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln	320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val	335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe	350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys	365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu	380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr	395	400	405

Glu Pro Trp Ala Glu Asp Ser Pro Pro Asp Gln Pro Pro Pro Ala
 410 415 420
 Ser Ala Arg Ser Ser Val Gly Glu Gly Glu Leu Gln Tyr Ala Ser
 425 430 435
 Leu Ser Phe Gln Met Val Lys Pro Trp Asp Ser Arg Gly Gln Glu
 440 445 450
 Ala Thr Asp Thr Glu Tyr Ser Glu Ile Lys Ile His Arg
 455 460

<210> 161
 <211> 739
 <212> DNA
 <213> Homo sapiens

<400> 161
 gacgccagtg gacctgccga ggtcgccgagc acagagctct ggagatgaag 50
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 cctggaggag gaggatatca cagggaacctg gtacgtgaag gccatggtgg 150
 tcgataagga ctttcgggag gacaggaggg ccaggaaggt gtccccaagt 200
 aaggtagacag ccttggggcgg tgggaagttg gaagccacgt tcaccttcac 250
 gaggggaggat cgggtgcaccc agaagaaaat cctgatgcgg aagacggagg 300
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350
 gagctgcccc ggagggaacca ctacatcttt tactgcaaa accagcacca 400
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450
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 tcggaggagg acattttcac gccctgcag acgggaagct gcgttccga 550
 acactaggca gccccgggt ctgcaacctc agagcccacc ctaccaccag 600
 acacagagcc cggaccacct ggacctacce tccagccatg accttccct 650
 gctcccacc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162
 <211> 170
 <212> PRT
 <213> Homo sapiens

<400> 162
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala
 1 5 10 15
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20										25					30				
Val	Lys	Ala	Met	Val	Val	Asp	Lys	Asp	Phe	Pro	Glu	Asp	Arg	Arg					
				35					40					45					
Pro	Arg	Lys	Val	Ser	Pro	Val	Lys	Val	Thr	Ala	Leu	Gly	Gly	Gly					
				50					55					60					
Lys	Leu	Glu	Ala	Thr	Phe	Thr	Phe	Met	Arg	Glu	Asp	Arg	Cys	Ile					
				65					70					75					
Gln	Lys	Lys	Ile	Leu	Met	Arg	Lys	Thr	Glu	Glu	Pro	Gly	Lys	Tyr					
				80					85					90					
Ser	Ala	Tyr	Gly	Gly	Arg	Lys	Leu	Met	Tyr	Leu	Gln	Glu	Leu	Pro					
				95					100					105					
Arg	Arg	Asp	His	Tyr	Ile	Phe	Tyr	Cys	Lys	Asp	Gln	His	His	Gly					
				110					115					120					
Gly	Leu	Leu	His	Met	Gly	Lys	Leu	Val	Gly	Arg	Asn	Ser	Asp	Thr					
				125					130					135					
Asn	Arg	Glu	Ala	Leu	Glu	Glu	Phe	Lys	Lys	Leu	Val	Gln	Arg	Lys					
				140					145					150					
Gly	Leu	Ser	Glu	Glu	Asp	Ile	Phe	Thr	Pro	Leu	Gln	Thr	Gly	Ser					
				155					160					165					
Cys	Val	Pro	Glu	His															
				170															

<210> 163
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-22
 <223> Synthetic construct.

<400> 163
 ggagatgaag accctgttcc tg 22

<210> 164
 <211> 26
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.

<400> 164
 ggagatgaag accctgttcc tgggtg 26

<210> 165
 <211> 21
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.

 <400> 165
 gtcctccgga aagtccttat c 21

 <210> 166
 <211> 25
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-25
 <223> Synthetic construct.

 <400> 166
 gcctagtgtt cgggaacaca gcttc 25

 <210> 167
 <211> 50
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

 <400> 167
 cagggaacctg gtacgtgaag gccatggtagg tcgataagga ctttccggag 50

 <210> 168
 <211> 45
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

 <400> 168
 ctgtccttca ccctggagga ggaggatata acagggacct ggtac 45

 <210> 169
 <211> 1204
 <212> DNA
 <213> Homo sapiens

 <400> 169

gtccgcaga tgcagaggtt gaggtggctg cgggactgga agtcateggg 50
 cajaggtctc acagcagcca aggaacctgg ggcgcgtccc tccccctccc 100
 agpccatgag gattctgcag ttaattctgc ttctctggc aacagggctt 150
 ctagggggag agaccaggat catcaagggg ttgagtgca agcctcactc 200
 ccagccctgg caggcagccc tgttcgagaa gacgcggcta ctctgtggg 250
 cgacgtcat cgcgccaga tggctctga cagcagccc ctgctcaag 300
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 ccttgaaata ttgtgactct gggaatgaca acacctgggt tgttctctgt 1100
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 aaaa 1204

<210> 170

<211> 250

<212> PRT

<213> Homo sapiens

<400> 170

Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu

1

5

10

15

<400> 171
ggtgaggga ctggaagfca tggg 25

<210> 172
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 172
ctccaggcca tgaggattct gcaq 24

<210> 173
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 173
cctctggtct gtaaccag 18

<210> 174
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 174
tctgtgatgt tgccggggla ggcg 24

<210> 175
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 175
cgtgtagaca ccaggctttc ggggtg 25

<210> 176
<211> 18
<212> DNA

<21> Artificial

<220>

<221> Artificial Sequence
<222> 1-18

<223> Synthetic construct.

<400> 176

cttggatga tectgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatccctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggcttcgagt gcaagcctca etc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

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gattcatlgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaag atagaagttt tgcacgtctc 150

agaaaactgc totaagacaa gcaagaaggg agacctacta aatgccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atgggttggt ctgggtgttg ggaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttaa acccccttca ttgcatatg gaaaggaagg ctatgcagaa 400

ggcagattc caccgagtc tacattgatt ttgagattg aactttatgc 450
 tgtgacaaa ggaacacgga gcattgagac atttaaacaa atagacatgg 500
 acaatgacag gcagctctct aaagccgaga taaacctcta ctgcaaaagg 550
 gaatttqaaa aagatgagaa gccacgtgac aagtcatatc aggatgcagt 600
 tttagaagat atttttaaga agaattacca tgatgggtgat ggcttcaitt 650
 ctcccaagga atacaatgta taccaacacg atgaactata gcataatitgt 700
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 ttgcaaacctt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
 aaaaaaa 907

<210> 180
 <211> 222
 <212> PRT
 <213> Homo sapiens

<400> 180

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Tyr	Leu	Trp	Gly	Leu	Phe	Thr	Ala	Gln	Arg	Gln	Lys	Lys	Glu	Glu
				20					25					30
Ser	Thr	Glu	Glu	Val	Lys	Ile	Glu	Val	Leu	His	Arg	Pro	Glu	Asn
				35					40					45
Cys	Ser	Lys	Thr	Ser	Lys	Lys	Gly	Asp	Leu	Leu	Asn	Ala	His	Tyr
				50					55					60
Asp	Gly	Tyr	Leu	Ala	Lys	Asp	Gly	Ser	Lys	Phe	Tyr	Cys	Ser	Arg
				65					70					75
Thr	Gln	Asn	Glu	Gly	His	Pro	Lys	Trp	Phe	Val	Leu	Gly	Val	Gly
				80					85					90
Gln	Val	Ile	Lys	Gly	Leu	Asp	Ile	Ala	Met	Thr	Asp	Met	Cys	Pro
				95					100					105
Gly	Glu	Lys	Arg	Lys	Val	Val	Ile	Pro	Pro	Ser	Phe	Ala	Tyr	Gly
				110					115					120
Lys	Glu	Gly	Tyr	Ala	Glu	Gly	Lys	Ile	Pro	Pro	Asp	Ala	Thr	Leu
				125					130					135
Ile	Phe	Glu	Ile	Glu	Leu	Tyr	Ala	Val	Thr	Lys	Gly	Pro	Arg	Ser
				140					145					150

Leu Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu
155 160 165

Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu
215 220

<210> 181

<211> 22

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-22

<223> Synthetic construct.

<400> 181

gtgtttctgct ggagccgatg cc 22

<210> 182

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 182

gacatggaca atgacagg 18

<210> 183

<211> 18

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 183

ccatttcagga tgtaggag 18

<210> 184

<211> 18

<212> DNA

<213> Artificial

<210> Artificial Sequence
 <211> 1-18
 <212> Synthetic construct.

 <400> 184
 gatgatctgcc accccaag 18

 <210> 185
 <211> 27
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-27
 <223> Synthetic construct.

 <400> 185
 gcactctgat atgaattgac acgtggc 27

 <210> 186
 <211> 24
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

 <400> 186
 tacaagaggg aagaggagtt gcac 24

 <210> 187
 <211> 52
 <212> DNA
 <213> Artificial

 <220>
 <221> Artificial Sequence
 <222> 1-52
 <223> Synthetic construct.

 <400> 187
 gccattatg acggctacct ggctaaagac ggctcgaaal tctactgcag 50
 cc 52

 <210> 188
 <211> 573
 <212> DNA
 <213> Homo sapiens

 <400> 188
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 ctctttggag ctgtgactca gaaaacaaa acttctgtg ctaagtgcgc 100

ccaatttct tctgtgttca ataactactca ctgcacctgc aacctatgat 150
 atacttttgg atctgggcag aaactattca cattccccctt ggagacatgt 200
 tggcagcgtc atggtggctc ggcctgttaa tcccagttct ttgggaagcc 250
 aagccaggtg gatcaactga ggtcaggagt ttgagaccag ccaggccaac 300
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350
 gtttcatgcc tgcaatccca gttactcggg aggctgagcc aggagaatcg 400
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450
 ctccagcatg gatgacagag caagactccg tcacaaaaag aaaagatagt 500
 ttcttgttcc atttcgcgac tgcctcttca gtgtttcctg ggatccccctc 550
 ccaataaaq tacttatatt etc 573

<210> 189
 <211> 74
 <212> PRT
 <213> Homo sapiens

<400> 189
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser
 1 5 10 15
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys
 20 25 30
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys
 35 40 45
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe
 50 55 60
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu
 65 70

<210> 190
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 190
 agggaccatt gcttcttcca ggcc 24

<210> 191
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 191
 cgttacatgt ctccaagggg aatg 24

<210> 192
 <211> 50
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-50
 <223> Synthetic construct.

<400> 192
 cctgtgctaa gtgcacccca aatgcttcc tgttcaataa cactcactgc 50

<210> 193
 <211> 1091
 <212> DNA
 <213> Homo sapiens

<400> 193
 caagcaggtc atcccttgg tgaccttcaa agagaagcag agagggcaga 50
 ggtggggggc acagggaaaag ggtgacctct gagattcccc ttttccccc 100
 gactttggaa gtgaccaccc atgggggctca gcatcttttt gctcctgtgt 150
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200
 gtgtgggggt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300
 gctcactgca ggggcagcag gtactgggtg cgcctggggg aacacagcct 350
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400
 cccatcccggt ctacctggga gcctcgacga gccacgagca cgaacctcgg 450
 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaacctct 500
 gcccttgccc aatgactgtg caaccgctgg caaccagttc cactctcag 550
 gctggggcat caccaaccac ccacggaacc cattcccgga tctgtccag 600
 tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650
 cgggagaatc acgagcaaca tgggtgtgtg aggcggcgtc ccggggcagg 700
 atgcctgcca qggtaattct gggggccccc tgggtgtgtg gggagtcctt 750
 caaggtctgg tgtctgggg gtctgtggg cctgtggac aagatggcat 800

ctgtggaatc tttacacata ttgtcaagta tgttgactgg atcccaatg: 850
 ttttgaggaa caactqaact gtttctcca cctcaccacc cacccttaa 900
 atttggtacc cctcttcccc tcagagcacc aatactctct ccactcacttc 950
 ccttagctcc actcttqttg gccttggaac ttcttggaac ttttaactct 1000
 tttacccttt ctaagaccca cgagcggggt gagagaagtg tgcataagtc 1050
 tggataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<10> 194
 <211> 248
 <212> PRT
 <213> Homo sapiens

<400> 194
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser
 1 5 10 15
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg
 20 25 30
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu
 35 40 45
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala
 50 55 60
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His
 65 70 75
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly
 80 85 90
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His
 95 100 105
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val
 110 115 120
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr
 125 130 135
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His
 140 145 150
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser
 155 160 165
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile
 170 175 180
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala
 185 190 195
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195
 <211> 1485
 <212> DNA
 <213> Homo sapiens

<400> 195
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 ctgcctcctc gcccgctccg cgaagccttg agccggcggg agccccgcgc 100
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150
 ggcttgctca aagccccgca ggagaggagg ctggccgaga tcaaccggga 200
 gtttctgtgt gaccagaaqt acagtgatga agagaacctt ccagaaaagc 250
 tcacagcctt caaagagaag tacatggagt ttgaacctgaa caatgaaggc 300
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350
 caagaccac ctggagatga aagagatgat ctgagaggtg acaggagggg 400
 tcagtgcac tatatccac ccagacttg tgaaatgat gctggggaaa 450
 ccgtcggttg tctcaagtt agtcatgatg ttggaaggaa aagccaacga 500
 gacagcccc aagccagttg gccccctcc agagagagac attgctagcc 550
 tgccctgagg acccgccctg gactccccag ccttcccacc ccatacctcc 600
 ctcccgatct tgcctgcctt ctlgacacac tglgatctct ctctctctca 650
 tttgtttggt cattgagggg ttgtttgtgt ttcatcaat gtctttgtaa 700
 agcacaatt atctgcctta aaggggctct gggtcgggga atctgagcc 750
 ttgggtcccc tccctctctt ctccctcct tccccgctcc ctgtgcagaa 800
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcagggagg 850
 ctccagcct gtgttccct cacttgagg aaccagcact ctccatcctt 900
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 gaccccaggc cactctgaga agaccttga gtagggacaa ggctgcaggg 1000
 cctctttcgg gtttcttgg acagtgcat ggttcagtg ctctggtgtc 1050

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 attccacacg tctttctcgc ctcaqfgatg tgaaggtggg aagcaaaagg 1150
 ptttgcattt gggagccctt caagaa-gta caagaaaggaa cctccacgtc 1200
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 gatactgagg ggaccaggat gggagaaatga ggagtaaaat gctcacggca 1400
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaa 1485

<210> 196

<211> 150

<212> PRT

<213> Homo sapiens

<400> 196

Met	Ser	Gly	Glu	Leu	Ser	Asn	Arg	Phe	Gln	Gly	Gly	Lys	Ala	Phe
1				5					10					15
Gly	Leu	Leu	Lys	Ala	Arg	Gln	Glu	Arg	Arg	Leu	Ala	Glu	Ile	Asn
				20					25					30
Arg	Glu	Phe	Leu	Cys	Asp	Gln	Lys	Tyr	Ser	Asp	Glu	Glu	Asn	Leu
				35					40					45
Pro	Glu	Lys	Leu	Thr	Ala	Phe	Lys	Glu	Lys	Tyr	Met	Glu	Phe	Asp
				50					55					60
Leu	Asn	Asn	Glu	Gly	Glu	Ile	Asp	Leu	Met	Ser	Leu	Lys	Arg	Met
				65					70					75
Met	Glu	Lys	Leu	Gly	Val	Pro	Lys	Thr	His	Leu	Glu	Met	Lys	Lys
				80					85					90
Met	Ile	Ser	Glu	Val	Thr	Gly	Gly	Val	Ser	Asp	Thr	Ile	Ser	Tyr
				95					100					105
Arg	Asp	Phe	Val	Asn	Met	Met	Leu	Gly	Lys	Arg	Ser	Ala	Val	Leu
				110					115					120
Lys	Leu	Val	Met	Met	Phe	Glu	Gly	Lys	Ala	Asn	Glu	Ser	Ser	Pro
				125					130					135
Lys	Pro	Val	Gly	Pro	Pro	Pro	Glu	Arg	Asp	Ile	Ala	Ser	Leu	Pro
				140					145					150

<210> 197

<211> 4842

<212> DNA

<213> Homo sapiens

440 197

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ggggctggcg cgcgcgtgcg cgcgcgcctg gcgcctggct tggcctggc 150
gagcgtcctg agtgggcctc cagcgcctcc ctgccccccc aagttatcct 200
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caccaggatc accaagatgg acttcgcctg gctcaagaa cctccagctc 350
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<210> 198
 <211> 1523
 <212> PRT
 <213> Homo sapiens

<400> 198
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 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro
 20 25 30
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val
 35 40 45
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro
 50 55 60
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg
 65 70 75
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu
 80 85 90
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe
 95 100 105
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys
 110 115 120
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu
 125 130 135
 Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg
 140 145 150
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp
 155 160 165

Asn Asn His Ile Ser Cys Ile Glu Asp Gly Ala Phe Arg Ala Leu	170	175	180
Arg Asp Leu Glu Ile Leu Thr Leu Asn Asn Asn Asn Ile Ser Arg	185	190	195
Ile Leu Val Thr Ser Phe Asn His Met Pro Lys Ile Arg Thr Leu	200	205	210
Arg Leu His Ser Asn His Leu Tyr Cys Asp Cys His Leu Ala Trp	215	220	225
Leu Ser Asp Trp Leu Arg Gln Arg Arg Thr Val Gly Gln Phe Thr	230	235	240
Leu Cys Met Ala Pro Val His Leu Arg Gly Phe Asn Val Ala Asp	245	250	255
Val Gln Lys Lys Glu Tyr Val Cys Pro Ala Pro His Ser Glu Pro	260	265	270
Pro Ser Cys Asn Ala Asn Ser Ile Ser Cys Pro Ser Pro Cys Thr	275	280	285
Cys Ser Asn Asn Ile Val Asp Cys Arg Gly Lys Gly Leu Met Glu	290	295	300
Ile Pro Ala Asn Leu Pro Glu Gly Ile Val Glu Ile Arg Leu Glu	305	310	315
Gln Asn Ser Ile Lys Ala Ile Pro Ala Gly Ala Phe Thr Gln Tyr	320	325	330
Lys Lys Leu Lys Arg Ile Asp Ile Ser Lys Asn Gln Ile Ser Asp	335	340	345
Ile Ala Pro Asp Ala Phe Gln Gly Leu Lys Ser Leu Thr Ser Leu	350	355	360
Val Leu Tyr Gly Asn Lys Ile Thr Glu Ile Ala Lys Gly Leu Phe	365	370	375
Asp Gly Leu Val Ser Leu Gln Leu Leu Leu Leu Asn Ala Asn Lys	380	385	390
Ile Asn Cys Leu Arg Val Asn Thr Phe Gln Asp Leu Gln Asn Leu	395	400	405
Asn Leu Leu Ser Leu Tyr Asp Asn Lys Leu Gln Thr Ile Ser Lys	410	415	420
Gly Leu Phe Ala Pro Leu Gln Ser Ile Gln Thr Leu His Leu Ala	425	430	435
Gln Asn Pro Phe Val Cys Asp Cys His Leu Lys Trp Leu Ala Asp	440	445	450
Tyr Leu Gln Asp Asn Pro Ile Glu Thr Ser Gly Ala Arg Cys Ser			

455	460	465
Ser Pro Arg Arg Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser	
470	475	480
Lys Lys Phe Arg Cys Ser Gly Ser Glu	Asp Tyr Arg Ser Arg Phe	
485	490	495
Ser Ser Glu Cys Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg	
500	505	510
Cys Glu Gly Thr Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg	
515	520	525
Ile Pro Ser His Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn	
530	535	540
Asp Asn Glu Val Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys	
545	550	555
Leu Pro Asn Leu Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys	
560	565	570
Glu Val Arg Glu Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu	
575	580	585
Leu Met Leu Thr Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val	
590	595	600
Phe Arg Gly Leu Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn	
605	610	615
Leu Ile Ser Cys Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser	
620	625	630
Val Arg Leu Leu Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr	
635	640	645
Pro Gly Ala Phe Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu	
650	655	660
Leu Ser Asn Pro Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly	
665	670	675
Lys Trp Leu Arg Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys	
680	685	690
Gln Lys Pro Phe Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala	
695	700	705
Ile Gln Asp Phe Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln	
710	715	720
Leu Ser Pro Arg Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val	
725	730	735
Val Arg Cys Ser Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met	
740	745	750

Pro	Lys	Asp	Val	Thr	Glu	Leu	Tyr	Leu	Glu	Gly	Asn	His	Leu	Thr	
				755					760						765
Ala	Val	Pro	Arg	Glu	Leu	Ser	Ala	Leu	Arg	His	Leu	Thr	Leu	Ile	
				770					775						780
Asp	Leu	Ser	Asn	Asn	Ser	Ile	Ser	Met	Leu	Thr	Asn	Tyr	Thr	Phe	
				785					790						795
Ser	Asn	Met	Ser	His	Leu	Ser	Thr	Leu	Ile	Leu	Ser	Tyr	Asn	Arg	
				800					805						810
Leu	Arg	Cys	Ile	Pro	Val	His	Ala	Phe	Asn	Gly	Leu	Arg	Ser	Leu	
				815					820						825
Arg	Val	Leu	Thr	Leu	His	Gly	Asn	Asp	Ile	Ser	Ser	Val	Pro	Glu	
				830					835						840
Gly	Ser	Phe	Asn	Asp	Leu	Thr	Ser	Leu	Ser	His	Leu	Ala	Leu	Gly	
				845					850						855
Thr	Asn	Pro	Leu	His	Cys	Asp	Cys	Ser	Leu	Arg	Trp	Leu	Ser	Glu	
				860					865						870
Trp	Val	Lys	Ala	Gly	Tyr	Lys	Glu	Pro	Gly	Ile	Ala	Arg	Cys	Ser	
				875					880						885
Ser	Pro	Glu	Pro	Met	Ala	Asp	Arg	Leu	Leu	Leu	Thr	Thr	Pro	Thr	
				890					895						900
His	Arg	Phe	Gln	Cys	Lys	Gly	Pro	Val	Asp	Ile	Asn	Ile	Val	Ala	
				905					910						915
Lys	Cys	Asn	Ala	Cys	Leu	Ser	Ser	Pro	Cys	Lys	Asn	Asn	Gly	Thr	
				920					925						930
Cys	Thr	Gln	Asp	Pro	Val	Glu	Leu	Tyr	Arg	Cys	Ala	Cys	Pro	Tyr	
				935					940						945
Ser	Tyr	Lys	Gly	Lys	Asp	Cys	Thr	Val	Pro	Ile	Asn	Thr	Cys	Ile	
				950					955						960
Gln	Asn	Pro	Cys	Gln	His	Gly	Gly	Thr	Cys	His	Leu	Ser	Asp	Ser	
				965					970						975
His	Lys	Asp	Gly	Phe	Ser	Cys	Ser	Cys	Pro	Leu	Gly	Phe	Glu	Gly	
				980					985						990
Gln	Arg	Cys	Glu	Ile	Asn	Pro	Asp	Asp	Cys	Glu	Asp	Asn	Asp	Cys	
				995					1000						1005
Glu	Asn	Asn	Ala	Thr	Cys	Val	Asp	Gly	Ile	Asn	Asn	Tyr	Val	Cys	
				1010					1015						1020
Ile	Cys	Pro	Pro	Asn	Tyr	Thr	Gly	Glu	Leu	Cys	Asp	Glu	Val	Ile	
				1025					1030						1035
Asp	His	Cys	Val	Pro	Glu	Leu	Asn	Leu	Cys	Gln	His	Glu	Ala	Lys	

1040	1045	1050
Cys Ile Pro Leu Asp Lys Gly Phe Ser Cys Glu Cys Val Pro Gly		
1055	1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala		
1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly		
1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu		
1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln		
1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu		
1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu		
1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu		
1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln		
1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp		
1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu		
1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val		
1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr		
1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys		
1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser		
1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala		
1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys		
1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala		
1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys		
1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser
 1340 1345 1350
 Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp
 1355 1360 1365
 Glu Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly
 1370 1375 1380
 Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu
 1385 1390 1395
 Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn
 1400 1405 1410
 Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser
 1415 1420 1425
 Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly
 1430 1435 1440
 Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg
 1445 1450 1455
 Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala
 1460 1465 1470
 Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln
 1475 1480 1485
 Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln
 1490 1495 1500
 Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu
 1505 1510 1515
 Glu Cys Gly Cys Leu Ala Cys Ser
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<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<21> Artificial Sequence
<22> 1-24
<23> Synthetic construct.

<400> 200
ttgttggeat tgaggaggag cagg 24

<210> 201
<211> 50
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-50
<223> Synthetic construct.

<400> 201
gagggcacag tcgaaataag cctagaacag aactccatca aagccatccc 50

<210> 202
<211> 753
<212> DNA
<213> Homo sapiens

<400> 202
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gaatctgcct ttccagttct gtctccggca ggctttgagg atgaaggctg 150
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgaatccaaa 200
atctacactc gttgcaaaact ggcaaaaata ttctcgaggg ctggcctgga 250
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300
agagcggcta caacaccaca gcccgcagcg tctggatga cggcagcatc 350
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450
atgacctcac agatgcaatt atctgtgcca ggaaaattgt taaagagaca 500
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cctgtccgag tggaaaaaag gctglgaggt ttcttaaact ggaactggac 600
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650
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gagggaaaat taagctatac ttttaagaaa ataaatattt ccatttaa 750
gtc 753

<210> 203
 <211> 148
 <212> PRT
 <213> Homo sapiens

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 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly
 35 40 45
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr
 50 55 60
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe
 65 70 75
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu
 80 85 90
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp
 95 100 105
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr
 110 115 120
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly
 125 130 135
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser
 140 145

<210> 204
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 204
 gcaggctttg aggatgaagg ctgc 24

<210> 205
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 205
 ctcttggtt gcttggtcag aggc 24

<210> 206
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 206
 ccagtcggac aggtctctcc cctc 24

<210> 207
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 207
 tcagtgaacca aggctgagca ggcg 24

<210> 208
 <211> 47
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-47
 <223> Synthetic construct.

<400> 208
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<210> 209
 <211> 1648
 <212> DNA
 <213> Homo sapiens

<400> 209
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 tattaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150
 ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200
 gcqgaagaag atccatthtt actgtcactt ccaqatctg cttctcacca 250

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<210> 210

<211> 323

ERT
me sapiens

110
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Glu Lys Phe Lys Leu Phe Thr Leu Val Ser Ala Cys Ile Pro Val
20 25 30
Phe Arg Leu Ala Arg Arg Arg Lys Lys Ile Leu Phe Tyr Cys His
35 40 45
Phe Pro Asp Leu Leu Leu Thr Lys Arg Asp Ser Phe Leu Lys Arg
50 55 60
Leu Tyr Arg Ala Pro Ile Asp Trp Ile Glu Glu Tyr Thr Thr Gly
65 70 75
Met Ala Asp Cys Ile Leu Val Asn Ser Gln Phe Thr Ala Ala Val
80 85 90
Phe Lys Glu Thr Phe Lys Ser Leu Ser His Ile Asp Pro Asp Val
95 100 105
Leu Tyr Pro Ser Leu Asn Val Thr Ser Phe Asp Ser Val Val Pro
110 115 120
Glu Lys Leu Asp Asp Leu Val Pro Lys Gly Lys Lys Phe Leu Leu
125 130 135
Leu Ser Ile Asn Arg Tyr Glu Arg Lys Lys Asn Leu Thr Leu Ala
140 145 150
Leu Glu Ala Leu Val Gln Leu Arg Gly Arg Leu Thr Ser Gln Asp
155 160 165
Trp Glu Arg Val His Leu Ile Val Ala Gly Gly Tyr Asp Glu Arg
170 175 180
Val Leu Glu Asn Val Glu His Tyr Gln Glu Leu Lys Lys Met Val
185 190 195
Gln Gln Ser Asp Leu Gly Gln Tyr Val Thr Phe Leu Arg Ser Phe
200 205 210
Ser Asp Lys Gln Lys Ile Ser Leu Leu His Ser Cys Thr Cys Val
215 220 225
Leu Tyr Thr Pro Ser Asn Glu His Phe Gly Ile Val Pro Leu Glu
230 235 240
Ala Met Tyr Met Gln Cys Pro Val Ile Ala Val Asn Ser Gly Gly
245 250 255
Pro Leu Glu Ser Ile Asp His Ser Val Thr Gly Phe Leu Cys Glu
260 265 270

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val
320

<210> 211
<211> 1554
<212> DNA
<213> Homo sapiens

<400> 211
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tctaccteta tccggcttcc agacaagctg caggaattcc agggattact 150
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggag 200
tttgcattgag ttcttggta atttgcattg gagatattgg cctgtggtct 250
ccttctggtt tggcaggcgc ctcttggta gtttgggcac tgttgatgta 300
ctgaagcagc atatcaatcc caataagaca tccgacctt ttgaaaccat 350
gctgaagtca ttattaaggt atcaatctgg tggtagcag gtgagtgaag 400
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450
agtaactttg ccttctctct aaagcttcca gaagaattat tagataaatg 500
gctctctac ccagagacct agcagtgcc cctcagccag catatgcttg 550
gttttgctat gaagtctgtt acacagatgg taatgggtag tacatttgaa 600
gatgatcagg aagtcattcg ctccagaag aatcatggca cagtittggtc 650
tgagattgga aaaggtttc tagatgggc acttgataaa aacatgactc 700
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750
aacatcataa aagaacgaaa aggaaggaaac ttcagtcaac atattttcat 800
tgactcttta gtacaaggga accttaatga ccaacagatc ctagaagaca 850
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900
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 aatcctttta taaccagta tcaactttgt atataaacac ctatttgtac 1550
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<210> 212

<211> 462

<212> PRT

<213> Homo sapiens

<400> 212

Met	Leu	Asp	Phe	Ala	Ile	Phe	Ala	Val	Thr	Phe	Leu	Leu	Ala	Leu
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Val	Gly	Ala	Val	Leu	Tyr	Leu	Tyr	Pro	Ala	Ser	Arg	Gln	Ala	Ala
				20					25					30
Gly	Ile	Pro	Gly	Ile	Thr	Pro	Thr	Glu	Glu	Lys	Asp	Gly	Asn	Leu
				35					40					45
Pro	Asp	Ile	Val	Asn	Ser	Gly	Ser	Leu	His	Glu	Phe	Leu	Val	Asn
				50					55					60
Leu	His	Glu	Arg	Tyr	Gly	Pro	Val	Val	Ser	Phe	Trp	Phe	Gly	Arg
				65					70					75
Arg	Leu	Val	Val	Ser	Leu	Gly	Thr	Val	Asp	Val	Leu	Lys	Gln	His
				80					85					90
Ile	Asn	Pro	Asn	Lys	Thr	Ser	Asp	Pro	Phe	Glu	Thr	Met	Leu	Lys
				95					100					105
Ser	Leu	Leu	Arg	Tyr	Gln	Ser	Gly	Gly	Gly	Ser	Val	Ser	Glu	Asn
				110					115					120
His	Met	Arg	Lys	Lys	Leu	Tyr	Glu	Asn	Gly	Val	Thr	Asp	Ser	Leu
				125					130					135
Lys	Ser	Asn	Phe	Ala	Leu	Leu	Leu	Lys	Leu	Ser	Glu	Glu	Leu	Leu

140	145	150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr	Gln His Val Pro Leu Ser	
155	160	165
Gln His Met Leu Gly Phe Ala Met Lys	Ser Val Thr Gln Met Val	
170	175	180
Met Gly Ser Thr Phe Glu Asp Asp Gln	Glu Val Ile Arg Phe Gln	
185	190	195
Lys Asn His Gly Thr Val Trp Ser Glu	Ile Gly Lys Gly Phe Leu	
200	205	210
Asp Gly Ser Leu Asp Lys Asn Met Thr	Arg Lys Lys Gln Tyr Glu	
215	220	225
Asp Ala Leu Met Gln Leu Glu Ser Val	Leu Arg Asn Ile Ile Lys	
230	235	240
Glu Arg Lys Gly Arg Asn Phe Ser Gln	His Ile Phe Ile Asp Ser	
245	250	255
Leu Val Gln Gly Asn Leu Asn Asp Gln	Gln Ile Leu Glu Asp Ser	
260	265	270
Met Ile Phe Ser Leu Ala Ser Cys Ile	Ile Thr Ala Lys Leu Cys	
275	280	285
Thr Trp Ala Ile Cys Phe Leu Thr Thr	Ser Glu Glu Val Gln Lys	
290	295	300
Lys Leu Tyr Glu Glu Ile Asn Gln Val	Phe Gly Asn Gly Pro Val	
305	310	315
Thr Pro Glu Lys Ile Glu Gln Leu Arg	Tyr Cys Gln His Val Leu	
320	325	330
Cys Gln Thr Val Arg Thr Ala Lys Leu	Thr Pro Val Ser Ala Gln	
335	340	345
Leu Gln Asp Ile Glu Gly Lys Ile Asp	Arg Phe Ile Ile Pro Arg	
350	355	360
Glu Thr Leu Val Leu Tyr Ala Leu Gly	Val Val Leu Gln Asp Pro	
365	370	375
Asn Thr Trp Pro Ser Pro His Lys Phe	Asp Pro Asp Arg Phe Asp	
380	385	390
Asp Glu Leu Val Met Lys Thr Phe Ser	Ser Leu Gly Phe Ser Gly	
395	400	405
Thr Gln Glu Cys Pro Glu Leu Arg Phe	Ala Tyr Met Val Thr Thr	
410	415	420
Val Leu Leu Ser Val Leu Val Lys Arg	Leu His Leu Leu Ser Val	
425	430	435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr
 455 460

<210> 213

<211> 759

<212> DNA

<213> Homo sapiens

<400> 213

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 cgtcatcacc ttattcttgt ccggggacag caacatacag gcttgcctgc 200
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 ttccctcggg aaactgcttc tgcctggagga tatgtgttgg aataattacg 650
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 tgttttctag taacattaag acttatatac agtttttaggg gacaattaaa 750
 aaaaaaaaa 759

<210> 214

<211> 140

<212> PRT

<213> Homo sapiens

<400> 214

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1				5				10						15
Leu	Ala	His	Leu	Val	Val	Val	Ile	Thr	Leu	Phe	Trp	Ser	Arg	Asp
			20					25						30
Ser	Asn	Ile	Gln	Ala	Cys	Leu	Pro	Leu	Thr	Phe	Thr	Pro	Glu	Glu
			35					40						45

17. Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr
 50 55 60
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val
 65 70 75
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His
 80 85 90
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp
 95 100 105
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu
 110 115 120
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu
 125 130 135
 Lys Lys Lys Pro Phe
 140

<210> 215
 <211> 697
 <212> DNA
 <213> Homo sapiens

<400> 215
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 gaccgggctt gctgcagccc catagtgcgc cggaacgagt ggaaggccct 150
 ggcatcagag tgcggccagc acctgagcct gcccttacgc tatgtggttg 200
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 catggccaaa aaccccatg tctctctctc caataaagat gtaqctc 697

<210> 216
 <211> 196
 <212> FRT

<210> Homo sapiens

<211> 216

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      5                                10                    15

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      20                    25                    30

Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu
      35                    40                    45

Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser
      50                    55                    60

His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln
      65                    70                    75

Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp
      80                    85                    90

Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val
      95                    100                   105

Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His
      110                   115                   120

Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr
      125                   130                   135

Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly
      140                   145                   150

Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr
      155                   160                   165

Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly
      170                   175                   180

Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser
      185                   190                   195

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Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

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tctatctggt catctgtggc caggatgatg gtctctccgg ctacagggac 150

cctgagcgtg atgaccaaga gggccagccc cggccccggg tgcctcggaa 200

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<210> 218
 <211> 252
 <212> PRT
 <213> Homo sapiens

<400> 218
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 Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg
 35 40 45
 Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met
 50 55 60
 Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala
 65 70 75
 Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro
 80 85 90
 Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe
 95 100 105
 Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly
 110 115 120
 Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln
 125 130 135
 His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro
 140 145 150
 Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile
 155 160 165
 Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu
 170 175 180
 Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro
 185 190 195
 Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp
 200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe
 215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr
 230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly
 245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

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<210> 220

<211> 201

<212> PRT

<213> Homo sapiens

<400> 220

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				20					25					30

Thr	Glu	Pro	Ile	Val	Leu	Glu	Gly	Lys	Cys	Leu	Val	Val	Cys	Asp
				35					40					45

Ser	Asn	Pro	Ala	Thr	Asp	Ser	Lys	Gly	Ser	Ser	Ser	Ser	Pro	Leu
				50					55					60

Gly	Ile	Ser	Val	Arg	Ala	Ala	Asn	Ser	Lys	Val	Ala	Phe	Ser	Ala	65	70	75
Val	Arg	Ser	Thr	Asn	His	Glu	Pro	Ser	Glu	Met	Ser	Asn	Lys	Thr	80	85	90
Arg	Ile	Ile	Tyr	Phe	Asp	Gln	Ile	Leu	Val	Asn	Val	Gly	Asn	Phe	95	100	105
Phe	Thr	Leu	Glu	Ser	Val	Phe	Val	Ala	Pro	Arg	Lys	Gly	Ile	Tyr	110	115	120
Ser	Phe	Ser	Phe	His	Val	Ile	Lys	Val	Tyr	Gln	Ser	Gln	Thr	Ile	125	130	135
Gln	Val	Asn	Leu	Met	Leu	Asn	Gly	Lys	Pro	Val	Ile	Ser	Ala	Phe	140	145	150
Ala	Gly	Asp	Lys	Asp	Val	Thr	Arg	Glu	Ala	Ala	Thr	Asn	Gly	Val	155	160	165
Leu	Leu	Tyr	Leu	Asp	Lys	Glu	Asp	Lys	Val	Tyr	Leu	Lys	Leu	Glu	170	175	180
Lys	Gly	Asn	Leu	Val	Gly	Gly	Trp	Gln	Tyr	Ser	Thr	Phe	Ser	Gly	185	190	195
Phe	Leu	Val	Phe	Pro	Leu										200		

<210> 221
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 221
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<210> 222
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 222
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<210> 223
 <211> 40

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-40
<223> Synthetic construct.

<400> 223
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<210> 224
<211> 902
<212> DNA
<213> Homo sapiens

<400> 224
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tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200
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<210> 225
<211> 257
<212> FRT

<213> Homo sapiens

<400> 225

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Arg	Ile	Ile	Phe	Leu	Ile	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	35	40	45	
Leu	Leu	Ile	Ser	Ser	Leu	Val	Trp	Phe	Met	Ala	Arg	Val	Ile	Ile	50	55	60	
Asp	Asn	Lys	Asp	Gly	Pro	Thr	Gln	Lys	Tyr	Leu	Leu	Ile	Phe	Gly	65	70	75	
Ala	Phe	Val	Ser	Val	Tyr	Ile	Gln	Glu	Met	Phe	Arg	Phe	Ala	Tyr	80	85	90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Ser	Glu	Gly	Leu	Lys	Ser	Ile	Asn	95	100	105	
Pro	Gly	Glu	Thr	Ala	Pro	Ser	Met	Arg	Leu	Leu	Ala	Tyr	Val	Ser	110	115	120	
Gly	Leu	Gly	Phe	Gly	Ile	Met	Ser	Gly	Val	Phe	Ser	Phe	Val	Asn	125	130	135	
Thr	Leu	Ser	Asp	Ser	Leu	Gly	Pro	Gly	Thr	Val	Gly	Ile	His	Gly	140	145	150	
Asp	Ser	Pro	Gln	Phe	Phe	Leu	Tyr	Ser	Ala	Phe	Met	Thr	Leu	Val	155	160	165	
Ile	Ile	Leu	Leu	His	Val	Phe	Trp	Gly	Ile	Val	Phe	Phe	Asp	Gly	170	175	180	
Cys	Glu	Lys	Lys	Lys	Trp	Gly	Ile	Leu	Leu	Ile	Val	Leu	Leu	Thr	185	190	195	
His	Leu	Leu	Val	Ser	Ala	Gln	Thr	Phe	Ile	Ser	Ser	Tyr	Tyr	Gly	200	205	210	
Ile	Asn	Leu	Ala	Ser	Ala	Phe	Ile	Ile	Leu	Val	Leu	Met	Gly	Thr	215	220	225	
Trp	Ala	Phe	Leu	Ala	Ala	Gly	Gly	Ser	Cys	Arg	Ser	Leu	Lys	Leu	230	235	240	
Cys	Leu	Leu	Cys	Gln	Asp	Lys	Asn	Phe	Leu	Leu	Tyr	Asn	Gln	Arg	245	250	255	

Ser Arg

<216> 226

<211> 3939
<212> DNA
<213> Homo sapiens

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<210> 227

<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Val	Glu	Ser	His	Leu	Gly	Val	Leu	Gly	Pro	Lys	Asn	Val	Ser	Gln
				20					25					30

Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Asp	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln	65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val	80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg	95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro	110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser	125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg	140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn	155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu	170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe	185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr	200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met	215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser	230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala	245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro	260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser	275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys	290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala	305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala			

320	325	330
Asp Arg Ala Cys Pro Glu Ser Gly	His Pro Arg Val Leu Ala	
335	340	345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr	Glu Gly Tyr Asn Tyr Gly	
350	355	360
Phe Phe Glu Asn Val Ser Gly Ser Thr	Asp Gly Leu Val Asp Ser	
365	370	375
Al Gly Thr Gly Asp Leu Ser Tyr Gly	Tyr Gln Gly Arg Ser Phe	
380	385	390
Glu Pro Val Gly Thr Arg Pro Arg Val	Asp Ser Met Ser Ser Val	
395	400	405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr	Asp Ile Asp Ser Asp Lys	
410	415	420
Asn Val Ile Arg Thr Lys Gln Tyr Leu	Tyr Val Ala Asp Leu Ala	
425	430	435
Arg Lys Asp Lys Arg Val Leu Arg Lys	Lys Tyr Gln Ile Tyr Phe	
440	445	450
Trp Asn Ile Ala Thr Ile Ala Val Phe	Tyr Ala Leu Pro Val Val	
455	460	465
Gln Leu Val Ile Thr Tyr Gln Thr Val	Val Asn Val Thr Gly Asn	
470	475	480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu	Cys Ala His Pro Leu Gly	
485	490	495
Asn Leu Ser Ala Phe Asn Asn Ile Leu	Ser Asn Leu Gly Tyr Ile	
500	505	510
Leu Leu Gly Leu Leu Phe Leu Leu Ile	Ile Leu Gln Arg Glu Ile	
515	520	525
Asn His Asn Arg Ala Leu Leu Arg Asn	Asp Leu Cys Ala Leu Glu	
530	535	540
Cys Gly Ile Pro Lys His Phe Gly Leu	Phe Tyr Ala Met Gly Thr	
545	550	555
Ala Leu Met Met Glu Gly Leu Leu Ser	Ala Cys Tyr His Val Cys	
560	565	570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp	Thr Ser Phe Met Tyr Met	
575	580	585
Ile Ala Gly Leu Cys Met Leu Lys Leu	Tyr Gln Lys Arg His Pro	
590	595	600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala	Tyr Ala Cys Leu Ala Ile	
605	610	615

Val	Ile	Phe	Ile	Ser	Val	Leu	Gly	Val	Val	Phe	Gly	Lys	Gly	Asn	
				620					625					630	
Thr	Ala	Phe	Trp	Ile	Val	Phe	Ser	Ile	Ile	His	Ile	Ile	Ala	Thr	
				635					640					645	
Leu	Leu	Leu	Ser	Thr	Gln	Leu	Tyr	Tyr	Met	Gly	Arg	Trp	Lys	Leu	
				650					655					660	
Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
				665					670					675	
Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
				680					685					690	
Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
				695					700					705	
Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
				710					715					720	
Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
				725					730					735	
Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
				740					745					750	
Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
				755					760					765	
Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
				770					775					780	
Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
				785					790					795	
His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
				800					805					810	
Phe	Leu	Val	Leu	Leu	Thr	Leu	Asp	Asp	Asp	Leu	Asp	Thr	Val	Gln	
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				830											

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 <212> DNA
 <213> Homo sapiens

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 ttggagctg gagggcctgt cctgaccatg gtccctgctt ggctgtggtt 150
 gctttgtgtc tccgtccccc aggtctctcc caaggcccag cctgcagagc 200

t g t t g t p r a a a t t t e a g a a a t a t g g t g g a a t t t t e e t t t a t a a e t g 250
 a a c a a g t t g c c g t g c c c c g t g a g g g g g g t g a a g g c c a g a t e g t g e t g t c 300
 a a g g a c t c a g g c a a g g c a a c t g a g g g c c c a t t t g e t a t g g a t c c a a t t 350
 a g g e t t e e t c e t g g t g a c c a g g c c e t g g a c c g a g a g a g c a g g c a g a g 400
 t a c c a g e t a c a g g t c a c c e t g g a g a t g c a g g a t g g a c a t g t e t t g t g g g 450
 t c c a g a g c e t g t g e t t g t g c a c t g a a g g a t g a g a a t g a c c a g t g c c c c 500
 a t t t e t e t c a a g c a t e t a c a g a g e t c g g c t g a g c c g g g g t a c c a g g c e t 550
 g g c a t c c c e t t e e t e t t e e t t g a g g e t t c a g a c c g g g a t g a g c c a g g c a c 600
 a g c c a a c t c g g a t e t t e g a t t c c a c a t c e t g a g c c a g g c t c c a g c c c a g c 650
 e t t c c c c a g a c a t g t t c a g c t g g a g c c t c g g e t g g g g g c t e t g g c c e t c 700
 a g c c c c a a g g g g a g c a c c a g c e t t g a c c a c g c c e t g g a g a g g a c e t a c c a 750
 g e t g t t g g t a c a g g t c a a g g a c a t g g g t g a c c a g g c c t c a g g c c a c c a g g 800
 c c a c t g c c a c c g t g g a a g t c t c a t c a t a g a g a g c a c c t g g g t g t c c e t a 850
 g a g c c t a t c c a c t g g c a g a g a a t c t c a a a g t c c t a t a c c c g c a c c a c a t 900
 g g c c c a g g t a c a c t g g a g t g g g g t g a t g t g c a c t a t c a c c t g g a g a g c c 950
 a t c c c c c g g g a c c c t t t g a a g t g a a t g c a g a g g g a a c c e t c t a c g t g a c c 1000
 a g a g a g c t g g a c a g a g a a g c c a g g c t g a g t a c c t g e t c c a g g t g c g g g c 1050
 t c a g a a t t c c a t g g c g a g g a c t a t g c g g c c c t e t g g a g c t g c a c g t g c 1100
 t g g t g a t g g a t g a g a a t g a c a a c g t g c c t a t e t g c c e t c c e g t g a c c c c 1150
 a c a g t c a g a t c c c t g a g e t c a g t c c a c c a g g t a c t g a a g t g a c t a g a c t 1200
 g t c a g c a g a g g a t g c a g a t g c c c c c g g t c c c c a a t t c c a c g t t g t g t 1250
 a t c a g e t e e t g a g c c c t g a g c e t g a g g a t g g g t a g a g g g g a g a g c e t t c 1300
 c a g g t g g a c c c a c t t c a g g c a g t g t g a c g c t g g g g g t g c t c c a c t c e g 1350
 a g c a g g c c a g a a c a t c e t g c t t e t g g t g e t g g c c a t g g a c c t g g c a g g c g 1400
 c a g a g g g t g g e t t c a g c a g c a c g t g t g a a g t c g a a g t c g c a g t c a c a g a t 1450
 a t c a a t g a t c a c g c c c c t g a g t t c a t c a c t t c c a g a t t g g g c c t a t a a g 1500
 c e t c e e t g a g g a t g t g g a g c c c g g g a c t e t g g t g g c c a t g c t a a c a g c c a 1550
 t t g a t g e t g a c c t e g a g c c c g c e t t c c g c c t e a t g g a t t t t g c c a t t g a g 1600
 a g g g g a g a c a g a a g g g a c t t t t g c c e t g g a t t g g g a g c c a g a c t e t g g 1650

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 gatgcacccc cccaagttag accaggagag ctacgaggee agtgtcccca 1850
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<210> 229

<211> 807

<212> PRT

<213> Homo sapiens

<400> 229

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Ala	Leu	Pro	Lys	Ala	Gln	Pro	Ala	Glu	Leu	Ser	Val	Glu	Val	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

20										25					30				
Glu	Asn	Tyr	Gly	Gly	Asn	Phe	Pro	Leu	Tyr	Leu	Thr	Lys	Leu	Pro					
				35					40					45					
Leu	Pro	Arg	Glu	Gly	Ala	Glu	Gly	Gln	Ile	Val	Leu	Ser	Gly	Asp					
				50					55					60					
Asp	Gly	Lys	Ala	Thr	Glu	Gly	Pro	Phe	Ala	Met	Asp	Pro	Asp	Ser					
				65					70					75					
Gly	Phe	Leu	Leu	Val	Thr	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Gln	Ala					
				80					85					90					
Glu	Tyr	Gln	Leu	Gln	Val	Thr	Leu	Glu	Met	Gln	Asp	Gly	His	Val					
				95					100					105					
Leu	Trp	Gly	Pro	Gln	Pro	Val	Leu	Val	His	Val	Lys	Asp	Glu	Asn					
				110					115					120					
Asp	Gln	Val	Pro	His	Phe	Ser	Gln	Ala	Ile	Tyr	Arg	Ala	Arg	Leu					
				125					130					135					
Ser	Arg	Gly	Thr	Arg	Pro	Gly	Ile	Pro	Phe	Leu	Phe	Leu	Glu	Ala					
				140					145					150					
Ser	Asp	Arg	Asp	Glu	Pro	Gly	Thr	Ala	Asn	Ser	Asp	Leu	Arg	Phe					
				155					160					165					
His	Ile	Leu	Ser	Gln	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Asp	Met	Phe					
				170					175					180					
Gln	Leu	Glu	Pro	Arg	Leu	Gly	Ala	Leu	Ala	Leu	Ser	Pro	Lys	Gly					
				185					190					195					
Ser	Thr	Ser	Leu	Asp	His	Ala	Leu	Glu	Arg	Thr	Tyr	Gln	Leu	Leu					
				200					205					210					
Val	Gln	Val	Lys	Asp	Met	Gly	Asp	Gln	Ala	Ser	Gly	His	Gln	Ala					
				215					220					225					
Thr	Ala	Thr	Val	Glu	Val	Ser	Ile	Ile	Glu	Ser	Thr	Trp	Val	Ser					
				230					235					240					
Leu	Glu	Pro	Ile	His	Leu	Ala	Glu	Asn	Leu	Lys	Val	Leu	Tyr	Pro					
				245					250					255					
His	His	Met	Ala	Gln	Val	His	Trp	Ser	Gly	Gly	Asp	Val	His	Tyr					
				260					265					270					
His	Leu	Glu	Ser	His	Pro	Pro	Gly	Pro	Phe	Glu	Val	Asn	Ala	Glu					
				275					280					285					
Gly	Asn	Leu	Tyr	Val	Thr	Arg	Glu	Leu	Asp	Arg	Glu	Ala	Gln	Ala					
				290					295					300					
Glu	Tyr	Leu	Leu	Gln	Val	Arg	Ala	Gln	Asn	Ser	His	Gly	Glu	Asp					
				305					310					315					

Val	Ala	Ala	Pro	Leu	Glu	Leu	His	Val	Leu	Val	Met	Asp	Glu	Asn	
				320					325					330	
Asp	Asn	Val	Ile	Cys	Pro	Pro	Arg	Asp	Pro	Thr	Val	Ser	Ile		
				335				340					345		
Ile	Glu	Leu	Ser	Pro	Pro	Gly	Thr	Glu	Val	Thr	Arg	Leu	Ser	Ala	
				350				355						360	
Glu	Asp	Ala	Asp	Ala	Pro	Gly	Ser	Pro	Asn	Ser	His	Val	Val	Tyr	
				365				370						375	
Glu	Leu	Leu	Ser	Pro	Glu	Pro	Glu	Asp	Gly	Val	Glu	Gly	Arg	Ala	
				380				385						390	
Ile	Gln	Val	Asp	Pro	Thr	Ser	Gly	Ser	Val	Thr	Leu	Gly	Val	Leu	
				395				400						405	
Pro	Leu	Arg	Ala	Gly	Gln	Asn	Ile	Leu	Leu	Leu	Val	Leu	Ala	Met	
				410				415						420	
Asp	Leu	Ala	Gly	Ala	Glu	Gly	Gly	Phe	Ser	Ser	Thr	Cys	Glu	Val	
				425				430						435	
Glu	Val	Ala	Val	Thr	Asp	Ile	Asn	Asp	His	Ala	Pro	Glu	Phe	Ile	
				440				445						450	
Thr	Ser	Gln	Ile	Gly	Pro	Ile	Ser	Leu	Pro	Glu	Asp	Val	Glu	Pro	
				455				460						465	
Gly	Thr	Leu	Val	Ala	Met	Leu	Thr	Ala	Ile	Asp	Ala	Asp	Leu	Glu	
				470				475						480	
Pro	Ala	Phe	Arg	Leu	Met	Asp	Phe	Ala	Ile	Glu	Arg	Gly	Asp	Thr	
				485				490						495	
Glu	Gly	Thr	Phe	Gly	Leu	Asp	Trp	Glu	Pro	Asp	Ser	Gly	His	Val	
				500				505						510	
Arg	Leu	Arg	Leu	Cys	Lys	Asn	Leu	Ser	Tyr	Glu	Ala	Ala	Pro	Ser	
				515				520						525	
His	Glu	Val	Val	Val	Val	Val	Gln	Ser	Val	Ala	Lys	Leu	Val	Gly	
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Pro	Gly	Pro	Gly	Pro	Gly	Ala	Thr	Ala	Thr	Val	Thr	Val	Leu	Val	
				545				550						555	
Glu	Arg	Val	Met	Pro	Pro	Pro	Lys	Leu	Asp	Gln	Glu	Ser	Tyr	Glu	
				560				565						570	
Ala	Ser	Val	Pro	Ile	Ser	Ala	Pro	Ala	Gly	Ser	Phe	Leu	Leu	Thr	
				575				580						585	
Ile	Gln	Pro	Ser	Asp	Pro	Ile	Ser	Arg	Thr	Leu	Arg	Phe	Ser	Leu	
				590				595						600	
Val	Asn	Asp	Ser	Glu	Gly	Trp	Leu	Cys	Ile	Glu	Lys	Phe	Ser	Gly	

	605	610	615
Leu Val His Thr	Ala Gln Ser Leu Gln Gly Ala Gln Pro Gly Asp		
	620	625	630
Thr Tyr Thr Val	Leu Val Glu Ala Gln Asp Thr Ala Leu Thr Leu		
	635	640	645
Ala Pro Val Pro	Ser Gln Tyr Leu Cys Thr Pro Arg Gln Asp His		
	650	655	660
Gly Leu Ile Val	Ser Gly Pro Ser Lys Asp Pro Asp Leu Ala Ser		
	665	670	675
Gly His Gly Pro	Tyr Ser Phe Thr Leu Gly Pro Asn Pro Thr Val		
	680	685	690
Gln Arg Asp Trp	Arg Leu Gln Thr Leu Asn Gly Ser His Ala Tyr		
	695	700	705
Leu Thr Leu Ala	Leu His Trp Val Glu Pro Arg Glu His Ile Ile		
	710	715	720
Pro Val Val Val	Ser His Asn Ala Gln Met Trp Gln Leu Leu Val		
	725	730	735
Arg Val Ile Val	Cys Arg Cys Asn Val Glu Gly Gln Cys Met Arg		
	740	745	750
Lys Val Gly Arg	Met Lys Gly Met Pro Thr Lys Leu Ser Ala Val		
	755	760	765
Gly Ile Leu Val	Gly Thr Leu Val Ala Ile Gly Ile Phe Leu Ile		
	770	775	780
Leu Ile Phe Thr	His Trp Thr Met Ser Arg Lys Lys Asp Pro Asp		
	785	790	795
Gln Pro Ala Asp	Ser Val Pro Leu Lys Ala Thr Val		
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<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 230

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<210> 231

<211> 24

<212> DNA

<213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> full
 <223> Synthetic oligonucleotide probe

<400> 231
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<210> 232
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 232
 agagtctgtc ccagctatct tgt 23

<210> 233
 <211> 2786
 <212> DNA
 <213> Homo sapiens

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 acttgaagct caattttctg aaatctccc cctccttcaa tcggcctgtg 200
 gatgtccttg tcccatctgt cagtctgcag gcatttaaat ccttcttgag 250
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 ggaaagggag ccagcgacaa ccttgcctcc gaagtgtacc atggacccca 850

cpeaaatleg gaagtggagg tgaatcaat ggtagatttc atcaaaaaac 900
 atggaaattt caagqcttc atcgaactgc aaactactc aaactctctc 950
 ctatataat atgggtactc agtcaaaaag ggtccagatg ccgaggaact 1000
 caacaagggtg gcgagqcttg cggccaaagc tctgqcttct ggtgcqgga 1050
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 agcatcacc cttctgggt ggcattgtc tetctacctc atttttagaa 1600
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 gaaaataatt tctttgagc acaaatctt gtagggatat cagtgaaggt 1800
 ctctccctcc ctctctctt gtttttttt tttttgagac agagtlttgc 1850
 tcttgttqcc caggtggag tgtgatggt cgatcttggc taccacaaac 1900
 ctctgcctcc tgggtcaag caattctct gctcagcct cttagagtagc 1950
 ttggtttata ggcacatgcc accatgcctg gctaattltg ttttttagt 2000
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 agccactgtg ccggcccggt cccctccttt tttaggcctg aalacaaagt 2150
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 ttactctct ctctccttg ttattcagtg tgaccaggat ggcgggaggg 2250
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<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

Met	Arg	Trp	Ile	Leu	Phe	Ile	Gly	Ala	Leu	Ile	Gly	Ser	Ser	Ile
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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile	170	175	180
Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala	185	190	195
Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser	200	205	210
Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro	215	220	225
Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys	230	235	240
Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro	245	250	255
Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp	260	265	270
Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu	275	280	285
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn	290	295	300
Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met	305	310	315
Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu	320	325	330
Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val	335	340	345
Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr	350	355	360
Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile	365	370	375
Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly	380	385	390
Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr	395	400	405
Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu	410	415	420

Tyr

<210> 235
 <211> 1743
 <212> DNA
 <213> Homo sapiens

-400> 235

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cccgcccttc ctccacaaag agcaccctg cctcacaggt gtartccctc 200
aacaccgaet ttgccttccg cclataccgc agyctggttt tggagacccc 250
gagtcagaac atctttctct cccctgtgag tgtctccact tccctggcca 300
tgtctccctt tggggccccc tcagtcacca agacccagat tctccagggc 350
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 acttactaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1743

<210> 236
 <211> 417
 <212> PRT
 <213> Homo sapiens

<400> 236
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys
 1 5 10 15
 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr
 20 25 30
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr
 35 40 45
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val
 50 55 60
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val
 65 70 75
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr
 80 85 90
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr
 95 100 105
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser
 110 115 120
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala
 125 130 135
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly
 140 145 150
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe
 155 160 165
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys
 170 175 180
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp
 185 190 195
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala

200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu Tyr Thr Arg Lys Asn Phe		
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr Val Gln Val Pro Met Met		
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly Val Asp Thr Glu Leu Asn		
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys Gly Asp Ala Val Ala Phe		
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met Arg Gln Leu Glu Gln Ala		
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp Ser His Ser Leu Gln Lys		
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg Phe Ser Ile Ser Ala Ser		
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys Met Gly Ile Gln Asn Ala		
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly Ile Ala Lys Arg Asp Ser		
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys Ala Val Leu Asp Val Ser		
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr Thr Thr Lys Phe Ile		
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr Phe Thr Val Ser Phe Asn		
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn Lys Ala Thr Asp Gly Ile		
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro Thr Lys Ser		
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-47
<223> Synthetic construct.

<400> 238
ctttgctggtt ggctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 239
tgactcgggg tctccaaaac cagc 24

<210> 240
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 240
ggtataggcg qaaggcaaag tcgg 24

<210> 241
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 241
ggcatcttac ctttatggag tactctttgc tgttgccctc tgtgctcc 48

<210> 242
<211> 2436
<212> DNA
<213> Homo sapiens

<400> 242
ggctgaccgt gctacattgc ctggaggaaq cctaagggaac ccaggcatcc 50

agctgccac gctgagtc aaatctcttc ccaggaaac aaacgttaga 100
 gacccagct cctggaagca ccagccttta tctcttcacc ttaagtc 150
 ctctctcaag aatcctctgt tctttgcct ctaaagctt ggtacateta 200
 gacccaggc atcttgcttt ccagccacaa agagacagat gaaatgcag 250
 aaggaaatg ttctccttat gtttggteta ctattgcatt tagaagctgc 300
 aacaaattcc aatgagacta gcacctctgc caaactgga tccagtgtga 350
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 agtggggtea gcacagccac catctcaggg tccagcgtga cctccaatgg 450
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 gcattcttca ggaaggaaga gacctgggca cccaagacct ggtttccttt 2100
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 aatactatat tgctcattta gctaagaaat aaatacatct catctaacac 2250
 acacgacaaa gagaagctgt gcttgccccg ggggtgggtat ctagctctga 2300
 gatgaactca gttataggag aaaacctcca tgctggactc calctggcat 2350
 tcaaaatctc cacagtaaaa tccaaagacc tcaaaaaaaaa aaaaaaaaaa 2400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2436

<210> 243
 <211> 596
 <212> PRT
 <213> Homo sapiens

<400> 243
 Met Lys Met Gln Lys Gly Asn Val Leu Leu Met Phe Gly Leu Leu
 1 5 10 15
 Leu His Leu Glu Ala Ala Thr Asn Ser Asn Glu Thr Ser Thr Ser
 20 25 30
 Ala Asn Thr Gly Ser Ser Val Ile Ser Ser Gly Ala Ser Thr Ala
 35 40 45
 Thr Asn Ser Gly Ser Ser Val Thr Ser Ser Gly Val Ser Thr Ala
 50 55 60
 Thr Ile Ser Gly Ser Ser Val Thr Ser Asn Gly Val Ser Ile Val
 65 70 75

Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	80	85	90
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	95	100	105
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	110	115	120
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	125	130	135
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	140	145	150
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	155	160	165
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	170	175	180
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	185	190	195
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	200	205	210
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	215	220	225
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	230	235	240
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	245	250	255
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	260	265	270
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	275	280	285
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	290	295	300
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	305	310	315
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	320	325	330
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	335	340	345
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	350	355	360
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala			

	365		370		375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380		385		390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395		400		405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410		415		420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425		430		435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440		445		450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455		460		465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470		475		480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485		490		495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500		505		510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515		520		525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530		535		540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545		550		555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560		565		570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575		580		585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590		595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

<400> 245
atcag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gt agaggttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggaccacaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaaatagca gcgtagcttc cctggctcct ctctgcatcc 50
tccccgacct tcccagcaat atgcatcttg caagtctggt cggctcctgc 100
tccctccttc tgctactggg ggccctgtct ggatgggagg ccagcagatga 150
ccccattgag aagggtcattg aagggatcaa ccgagggctg agcaatgcag 200
agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250
gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300
ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350
tggaacaagg tgcccatgag atcaaccatg gtattggaca agcaggaaaag 400
gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450
gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtcaccagg 500
ctgggaagga agcagagaaa ctgggccaag gggtaacca tgctgctgac 550
caggctggaa aggaagtggg gaagcttggc caaggtgccc accatgctgc 600

tttttttt ggggaaggagc tgcagaatgc tcatgaatggg gtaaccaag 650
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 tttttttt tttt aaggaaggggc cacaaccacg ccgttagcct ctgggggcctc 750
 cttttttt cgttttcatca accttccgcg cctgtggagg agcgtcgcga 800
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 gttttttt cactgacat gacctggagg gggtgggggt gggggacagg 900
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<210> 248

<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

Met	His	Leu	Ala	Arg	Leu	Val	Gly	Ser	Cys	Ser	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu
				20					25					30
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg
				35					40					45
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His
				50					55					60
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met
				65					70					75
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu
				80					85					90
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile
				95					100					105
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn
				110					115					120
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln
				125					130					135
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys
				140					145					150
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu
				155					160					165
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala
				170					175					180

Asn	Glu	Leu	Gln	Asn	Ala	His	Asn	Gly	Val	Asn	Gln	Ala	Ser
			185					190					195
Thr	Ala	Asn	Gln	Leu	Leu	Asn	Gly	Asn	His	Gln	Ser	Gly	Ser
			200					205					210
Pro	His	Gln	Gly	Gly	Ala	Thr	Thr	Thr	Pro	Leu	Ala	Ser	Gly
			215					220					225
Ala	Ser	Val	Asn	Thr	Pro	Phe	Ile	Asn	Leu	Pro	Ala	Leu	Trp
			230					235					240
Ser	Val	Ala	Asn	Ile	Met	Pro							
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<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 249

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<210> 250

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 250

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<210> 251

<211> 43

<212> DNA

<213> Artificial

<220>

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<222> 1-43

<223> Synthetic construct.

<400> 251

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<210> 252

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<212> DNA

<213> Homo sapiens

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<210> 253

<211> 837

<212> PRT

<213> Homo sapiens

<400> 253

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				20					25					30
Leu	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Pro	Pro	Thr	Trp	Ala	Leu	Ser
				35					40					45
Pro	Arg	Ile	Ser	Leu	Pro	Leu	Gly	Ser	Glu	Glu	Arg	Pro	Phe	Leu
				50					55					60
Arg	Phe	Glu	Ala	Glu	His	Ile	Ser	Asn	Tyr	Thr	Ala	Leu	Leu	Leu
				65					70					75
Ser	Arg	Asp	Gly	Arg	Thr	Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Leu

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	Leu Ser Ser Asn Leu Ser Phe	Leu Pro Gly Gly Glu Tyr	
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Gln	Leu Leu Trp Gly Ala Asp Ala	Glu Lys Lys Gln Gln Cys	
	110	115	120
Leu	Ile Lys Gly Lys Asp Pro Gln Arg	Asp Cys Gln Asn Tyr Ile	
	125	130	135
Lys	Ile Leu Leu Pro Leu Ser Gly Ser	His Leu Phe Thr Cys Gly	
	140	145	150
Thr	Ala Ala Phe Ser Pro Met Cys Thr	Tyr Ile Asn Met Glu Asn	
	155	160	165
Phe	Thr Leu Ala Arg Asp Glu Lys Gly	Asn Val Leu Leu Glu Asp	
	170	175	180
Gly	Lys Gly Arg Cys Pro Phe Asp Pro	Asn Phe Lys Ser Thr Ala	
	185	190	195
Leu	Val Val Asp Gly Glu Leu Tyr Thr	Gly Thr Val Ser Ser Phe	
	200	205	210
Gln	Gly Asn Asp Pro Ala Ile Ser Arg	Ser Gln Ser Leu Arg Pro	
	215	220	225
Thr	Lys Thr Glu Ser Ser Leu Asn Trp	Leu Gln Asp Pro Ala Phe	
	230	235	240
Val	Ala Ser Ala Tyr Ile Pro Glu Ser	Leu Gly Ser Leu Gln Gly	
	245	250	255
Asp	Asp Asp Lys Ile Tyr Phe Phe Phe	Ser Glu Thr Gly Gln Glu	
	260	265	270
Phe	Glu Phe Phe Glu Asn Thr Ile Val	Ser Arg Ile Ala Arg Ile	
	275	280	285
Cys	Lys Gly Asp Glu Gly Gly Glu Arg	Val Leu Gln Gln Arg Trp	
	290	295	300
Thr	Ser Phe Leu Lys Ala Gln Leu Leu	Cys Ser Arg Pro Asp Asp	
	305	310	315
Gly	Phe Pro Phe Asn Val Leu Gln Asp	Val Phe Thr Leu Ser Pro	
	320	325	330
Ser	Pro Gln Asp Trp Arg Asp Thr Leu	Phe Tyr Gly Val Phe Thr	
	335	340	345
Ser	Gln Trp His Arg Gly Thr Thr Glu	Gly Ser Ala Val Cys Val	
	350	355	360
Phe	Thr Met Lys Asp Val Gln Arg Val	Phe Ser Gly Leu Tyr Lys	
	365	370	375

Val	Asn	Arg	Glu	Thr	Gln	Gln	Trp	Tyr	Thr	Val	Thr	His	Ile	
			380					385					390	
Val	Ile	Thr	Pro	Arg	Pro	Gly	Ala	Cys	Ile	Thr	Asn	Ser	Ala	Arg
				395					400					405
Gln	Arg	Lys	Ile	Asn	Ser	Ser	Leu	Gln	Leu	Ile	Asp	Arg	Val	Leu
				410					415					420
Asn	Phe	Leu	Lys	Asp	His	Phe	Leu	Met	Asp	Gly	Gln	Val	Arg	Ser
				425					430					435
Arg	Met	Leu	Leu	Leu	Gln	Pro	Gln	Ala	Arg	Tyr	Gln	Arg	Val	Ala
				440					445					450
Val	His	Arg	Val	Pro	Gly	Leu	His	His	Thr	Tyr	Asp	Val	Leu	Phe
				455					460					465
Leu	Gly	Thr	Gly	Asp	Gly	Arg	Leu	His	Lys	Ala	Val	Ser	Val	Gly
				470					475					480
Pro	Arg	Val	His	Ile	Ile	Glu	Glu	Leu	Gln	Ile	Phe	Ser	Ser	Gly
				485					490					495
Gln	Pro	Val	Gln	Asn	Leu	Leu	Leu	Asp	Thr	His	Arg	Gly	Leu	Leu
				500					505					510
Tyr	Ala	Ala	Ser	His	Ser	Gly	Val	Val	Gln	Val	Pro	Met	Ala	Asn
				515					520					525
Cys	Ser	Leu	Tyr	Arg	Ser	Cys	Gly	Asp	Cys	Leu	Leu	Ala	Arg	Asp
				530					535					540
Pro	Tyr	Cys	Ala	Trp	Ser	Gly	Ser	Ser	Cys	Lys	His	Val	Ser	Leu
				545					550					555
Tyr	Gln	Pro	Gln	Leu	Ala	Thr	Arg	Pro	Trp	Ile	Gln	Asp	Ile	Glu
				560					565					570
Gly	Ala	Ser	Ala	Lys	Asp	Leu	Cys	Ser	Ala	Ser	Ser	Val	Val	Ser
				575					580					585
Pro	Ser	Phe	Val	Pro	Thr	Gly	Glu	Lys	Pro	Cys	Glu	Gln	Val	Gln
				590					595					600
Phe	Gln	Pro	Asn	Thr	Val	Asn	Thr	Leu	Ala	Cys	Pro	Leu	Leu	Ser
				605					610					615
Asn	Leu	Ala	Thr	Arg	Leu	Trp	Leu	Arg	Asn	Gly	Ala	Pro	Val	Asn
				620					625					630
Ala	Ser	Ala	Ser	Cys	His	Val	Leu	Pro	Thr	Gly	Asp	Leu	Leu	Leu
				635					640					645
Val	Gly	Thr	Gln	Gln	Leu	Gly	Glu	Phe	Gln	Cys	Trp	Ser	Leu	Glu
				650					655					660
Glu	Gly	Phe	Gln	Gln	Leu	Val	Ala	Ser	Tyr	Cys	Pro	Glu	Val	Val

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Asp	Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val	Pro	
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Ile	Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly	Lys	
	695		700		705
Trp	Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu	Val	
	710		715		720
Met	Lys Thr	Leu Phe Val Leu Ala Val	Leu Leu Pro Val Leu	Phe	
	725		730		735
Leu	Leu Tyr	Arg His Arg Asn Ser Met	Lys Val Phe Leu Lys	Gln	
	740		745		750
Gly	Glu Cys	Ala Ser Val His Pro Lys	Thr Cys Pro Val Val	Leu	
	755		760		765
Pro	Pro Glu	Thr Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser	Thr	
	770		775		780
Pro	Leu Asp	His Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro	Pro	
	785		790		795
Gly	Ala Arg	Val Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser	Ile	
	800		805		810
Gln	Asp Ser	Phe Val Glu Val Ser Pro	Val Cys Pro Arg Pro	Arg	
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 ttcattttaga tttcaaacag tgatagactt gccattttaa tacacgtcat 4400
 tggagggctg cgtatttgta aatagcctga tgcctatttg gaaaaataaa 4450
 ccagtgaaca atattttct attgtacttt tcgaaccatt ttgtctcatt 4500

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 aaacacgaaa aaa 4563

<211> 260

<211> 802

<212> FRT

<213> Homo sapiens

<400> 260

Met	Ala	Ala	Arg	Gly	Arg	Arg	Ala	Trp	Leu	Ser	Val	Leu	Leu	Gly	1	5	10	15
Leu	Val	Leu	Gly	Phe	Val	Leu	Ala	Ser	Arg	Leu	Val	Leu	Pro	Arg	20	25	30	
Ala	Ser	Glu	Leu	Lys	Arg	Ala	Gly	Pro	Arg	Arg	Arg	Ala	Ser	Pro	35	40	45	
Glu	Gly	Cys	Arg	Ser	Gly	Gln	Ala	Ala	Ala	Ser	Gln	Ala	Gly	Gly	50	55	60	
Ala	Arg	Gly	Asp	Ala	Arg	Gly	Ala	Gln	Leu	Trp	Pro	Pro	Gly	Ser	65	70	75	
Asp	Pro	Asp	Gly	Gly	Pro	Arg	Asp	Arg	Asn	Phe	Leu	Phe	Val	Gly	80	85	90	
Val	Met	Thr	Ala	Gln	Lys	Tyr	Leu	Gln	Thr	Arg	Ala	Val	Ala	Ala	95	100	105	
Tyr	Arg	Thr	Trp	Ser	Lys	Thr	Ile	Pro	Gly	Lys	Val	Gln	Phe	Phe	110	115	120	
Ser	Ser	Glu	Gly	Ser	Asp	Thr	Ser	Val	Pro	Ile	Pro	Val	Val	Pro	125	130	135	
Leu	Arg	Gly	Val	Asp	Asp	Ser	Tyr	Pro	Pro	Gln	Lys	Lys	Ser	Phe	140	145	150	
Met	Met	Leu	Lys	Tyr	Met	His	Asp	His	Tyr	Leu	Asp	Lys	Tyr	Glu	155	160	165	
Trp	Phe	Met	Arg	Ala	Asp	Asp	Asp	Val	Tyr	Ile	Lys	Gly	Asp	Arg	170	175	180	
Leu	Glu	Asn	Phe	Leu	Arg	Ser	Leu	Asn	Ser	Ser	Glu	Pro	Leu	Phe	185	190	195	
Leu	Gly	Gln	Thr	Gly	Leu	Gly	Thr	Thr	Glu	Glu	Met	Gly	Lys	Leu	200	205	210	
Ala	Leu	Glu	Pro	Gly	Glu	Asn	Phe	Cys	Met	Gly	Gly	Pro	Gly	Val	215	220	225	
Ile	Met	Ser	Arg	Glu	Val	Leu	Arg	Arg	Met	Val	Pro	His	Ile	Gly	230	235	240	

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

530	535	540
Leu Gly Arg Phe Asp Met Phe Val Arg	Phe Met Gly Asn Phe Glu	
545	550	555
Lys Thr Cys Leu Ile Pro Asn Gln Asn	Val Lys Leu Val Val Leu	
560	565	570
Leu Phe Asn Ser Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val Glu	
575	580	585
Leu Met Arg Asp Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met Gln	
590	595	600
Ile Leu Pro Val Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu Glu	
605	610	615
Val Gly Ser Ser Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe Cys	
620	625	630
Asp Val Asp Leu Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys Arg	
635	640	645
Ala Asn Thr Val Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile Phe	
650	655	660
Ser Gln Tyr Asp Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro Ser	
665	670	675
Asp Asn His Phe Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg Asn	
680	685	690
Tyr Gly Phe Gly Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val Arg	
695	700	705
Val Gly Gly Phe Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu Asp	
710	715	720
Val Asp Leu Phe Asn Lys Val Val Gln	Ala Gly Leu Lys Thr Phe	
725	730	735
Arg Ser Gln Glu Val Gly Val Val His	Val His His Pro Val Phe	
740	745	750
Cys Asp Pro Asn Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu Gly	
755	760	765
Ser Lys Ala Ser Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu Met	
770	775	780
Trp Leu Glu Lys Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn Asn	
785	790	795
Asn Gly Ser Val Arg Thr Ala		
800		

<210> 261
 <211> 24

<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 261
gtgccactac ggggtgtgga cgac 24

<210> 262
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 262
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<210> 263
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 263
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<210> 264
<211> 1419
<212> DNA
<213> Homo sapiens

<400> 264
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tgacaccttc ccttcgggcc ttgagggtcc cagcctggtg gccccaggac 100
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tcttctagt tgcgtttttg ctatggcctt cgtctgtgcc ggccttaccg 200
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

ttttacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450
 ; ttttacc ggaatatgga aagaaaaaac acacggaaaag taccocattc 500
 ttttacc aaccaaacaa tgtttccatt gttttgcattg cagaggaacc 550
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 cctttgttta cctcatataa gtcacctgic accactttag ataagagcac 700
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 aacaagtaat aaaattgatg acatcgaaac tgttattaac atgctgtgta 1050
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 tagatcaagg agagtcacag ccttattaaa agttttattaa acaataatat 1200
 aaaaatttta aacctacttg atattccata acaaagctga ttttaagcaa 1250
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 ataaaaatat tttctattgt agttcaaatg tgccaacatc tttatgtgtc 1350
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<210> 265

<211> 350

<212> PRT

<213> Homo sapiens

<400> 265

Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser
 1 5 10 15

Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu
 20 25 30

Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg
 35 40 45

Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser

	50		55		60
His Val Tyr Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys	65		70		75
Leu Val Thr His Gly Asp Ala Ser Thr Glu Asn Asp Val Leu	80		85		90
Thr Asn Pro Ile Ser Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly	95		100		105
Phe Thr Pro Glu Ile Gly Lys Lys Lys His Thr Glu Ser Thr Pro	110		115		120
Phe Trp Ser Ile Lys Pro Asn Asn Val Ser Ile Val Leu His Ala	125		130		135
Glu Glu Pro Tyr Ile Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu	140		145		150
Pro Ala Ala Lys Gln Thr Glu Ala Pro Arg Met Leu Pro Val Val	155		160		165
Thr Glu Ser Ser Thr Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro	170		175		180
Val Thr Thr Leu Asp Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu	185		190		195
Ser Glu Asp Val Pro Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys	200		205		210
Pro Glu Glu Phe Gly Lys His Pro Glu Ser Trp Asn Asn Asp Asp	215		220		225
Ile Leu Lys Lys Ile Leu Asp Ile Asn Ser Gln Val Gln Gln Ala	230		235		240
Leu Leu Ser Asp Thr Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu	245		250		255
Ala Ser Lys Asp His Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala	260		265		270
Ala Glu His Lys Leu Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro	275		280		285
Val Gly Arg Thr Ser Asn Lys Ile Asp Asp Ile Glu Thr Val Ile	290		295		300
Asn Met Leu Cys Asn Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp	305		310		315
Ile Lys Cys Val Pro Pro Glu Met Arg Glu Lys Ala Ala Thr Val	320		325		330
Phe Asn Thr Leu Lys Asn Met Cys Arg Ser Arg Arg Val Thr Ala	335		340		345

Ileu Leu Lys Val Tyr
 350

210 266

1403

1122 DNA

213 Homo sapiens

1400 266

cggctcagac ggctcgagtg aagagccctc ccacggctcc tgcgcctgag 50
 acagctggcc tgacctccaa atcctccatc caccctgct gtcctctgtt 100
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 ttltggtctc agtttctacg agctgggtgc aggacagtgg caagtccactg 200
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 gggaatctaa gcagatgcc aagtatcgag ggagaactga gtttgtgaag 400
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<210> 267

<211> 466

<212> PRT

<213> Homo sapiens

<400> 267

Met	Ala	Phe	Val	Leu	Ile	Leu	Val	Leu	Ser	Phe	Tyr	Glu	Leu	Val
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Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

	20	25	30
1	Gly Glu Asp Ala Val Phe Ser Cys Ser Leu Phe Pro Glu		
	35	40	45
2	Leu Ala Glu Ala Met Glu Val Arg Phe Phe Arg Asn Gln Phe		
	50	55	60
3	Val Val His Leu Tyr Arg Asp Gly Glu Asp Trp Glu Ser		
	65	70	75
4	Met Pro Gln Tyr Arg Gly Arg Thr Glu Phe Val Lys Asp		
	80	85	90
5	Ile Ala Gly Gly Arg Val Ser Leu Arg Leu Lys Asn Ile Thr		
	95	100	105
6	Ser Asp Ile Gly Leu Tyr Gly Cys Trp Phe Ser Ser Gln Ile		
	110	115	120
7	Tyr Asp Glu Glu Ala Thr Trp Glu Leu Arg Val Ala Ala Leu Gly		
	125	130	135
8	Ser Leu Pro Leu Ile Ser Ile Val Gly Tyr Val Asp Gly Gly Ile		
	140	145	150
9	Gln Leu Leu Cys Leu Ser Ser Gly Trp Phe Pro Gln Pro Thr Ala		
	155	160	165
10	Lys Trp Lys Gly Pro Gln Gly Gln Asp Leu Ser Ser Asp Ser Arg		
	170	175	180
11	Ala Asn Ala Asp Gly Tyr Ser Leu Tyr Asp Val Glu Ile Ser Ile		
	185	190	195
12	Ile Val Gln Glu Asn Ala Gly Ser Ile Leu Cys Ser Ile His Leu		
	200	205	210
13	Ala Glu Gln Ser His Glu Val Glu Ser Lys Val Leu Ile Gly Glu		
	215	220	225
14	Thr Phe Phe Gln Pro Ser Pro Trp Arg Leu Ala Ser Ile Leu Leu		
	230	235	240
15	Gly Leu Leu Cys Gly Ala Leu Cys Gly Val Val Met Gly Met Ile		
	245	250	255
16	Ile Val Phe Phe Lys Ser Lys Gly Lys Ile Gln Ala Glu Leu Asp		
	260	265	270
17	Trp Arg Arg Lys His Gly Gln Ala Glu Leu Arg Asp Ala Arg Lys		
	275	280	285
18	His Ala Val Glu Val Thr Leu Asp Pro Glu Thr Ala His Pro Lys		
	290	295	300
19	Leu Cys Val Ser Asp Leu Lys Thr Val Thr His Arg Lys Ala Pro		
	305	310	315

Val	Ala	Val	Pro	His	Ser	Glu	Lys	Arg	Phe	Thr	Arg	Lys	Ser	Val
						320				325				330
Val	Ala	Ser	Gln	Gly	Phe	Gln	Ala	Gly	Arg	His	Tyr	Trp	Glu	Val
						335				340				345
Asp	Val	Gly	Gln	Asn	Val	Gly	Trp	Tyr	Val	Gly	Val	Cys	Arg	Asp
						350				355				360
Asp	Val	Asp	Arg	Gly	Lys	Asn	Asn	Val	Thr	Leu	Ser	Pro	Asn	Asn
						365				370				375
Gly	Tyr	Trp	Val	Leu	Arg	Leu	Thr	Thr	Glu	His	Leu	Tyr	Phe	Thr
						380				385				390
Phe	Asn	Pro	His	Phe	Ile	Ser	Leu	Pro	Pro	Ser	Thr	Pro	Pro	Thr
						395				400				405
Arg	Val	Gly	Val	Phe	Leu	Asp	Tyr	Glu	Gly	Gly	Thr	Ile	Ser	Phe
						410				415				420
Phe	Asn	Thr	Asn	Asp	Gln	Ser	Leu	Ile	Tyr	Thr	Leu	Leu	Thr	Cys
						425				430				435
Gln	Phe	Glu	Gly	Leu	Leu	Arg	Pro	Tyr	Ile	Gln	His	Ala	Met	Tyr
						440				445				450
Asp	Glu	Glu	Lys	Gly	Thr	Pro	Ile	Phe	Ile	Cys	Pro	Val	Ser	Trp
						455				460				465

Gly

<210> 268
 <211> 2103
 <212> DNA
 <213> Homo sapiens

<400> 268
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 tgtcatittac aactgacaaa ctatatgctg agtttggcag agaggcttct 250
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300
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 tgttttacct gaaaagctgc aagatgctgt aggacccctt aaagtagatc 500

tttttagt taatat'aaa aaaatcaaca agacagaaac agacagctat 550
 ctatcattt gctggggaac acgaagaaqt aaaactctag gtcagagctt 600
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 tttttaggc ttgtgagtgc tgcacactgt ttacaaacat ataagaaccc 750
 tgggaatgg actgcttcc tggagtaga aataaaacct tcgaaaatga 800
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 aalaccaatc acttcatcat ttaggaagta tgggaactaa gtttaggaag 1900
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 ... 2103

216 169
 211 423
 212 PRT
 Homo sapiens

216 169
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys
 1 5 10 15
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile
 20 25 30
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr
 35 40 45
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr
 50 55 60
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn
 65 70 75
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 80 85 90
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val
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 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu
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 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp
 125 130 135
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val
 140 145 150
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile
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 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr
 170 175 180
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly
 185 190 195
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln
 200 205 210
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr
 215 220 225

Thr	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro	230	235	240	
Ala	Asp	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys	245	250	255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys	260	265	270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser	275	280	285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp	290	295	300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly	305	310	315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg	320	325	330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro	335	340	345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly	350	355	360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly	365	370	375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly	380	385	390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly	395	400	405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys	410	415	420

Thr Gly Ile

<210> 270

<211> 1170

<212> DNA

<213> Homo sapiens

<400> 270

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<211> 238

<212> PRT

<213> Homo sapiens

<400> 271

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			20					25					30	
Glu	Glu	Ala	Asp	Glu	Thr	Glu	Thr	Ala	Trp	Pro	Pro	Leu	Pro	Ala
			35					40					45	
Val	Pro	Cys	Asp	Tyr	Asp	His	Cys	Arg	His	Leu	Gln	Val	Pro	Cys
			50					55					60	
Lys	Glu	Leu	Gln	Arg	Val	Gly	Pro	Ala	Ala	Cys	Leu	Cys	Pro	Gly
			65					70					75	

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
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Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
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Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
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Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
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Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
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Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
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Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
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<211> 2397

<212> DNA

<213> Homo sapiens

<400> 272

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 <211> 305
 <212> PRT
 <213> Homo sapiens

<400> 273

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Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu	35	40	45	
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe	50	55	60	
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile	65	70	75	
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu	80	85	90	
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys	95	100	105	
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met	110	115	120	
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met	125	130	135	
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp	140	145	150	
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe	155	160	165	
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser				

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200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
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Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
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Glu Met Glu Glu Leu		
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 <211> 2063
 <212> DNA
 <213> Homo sapiens

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265

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				275					280					285
Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly	Thr
				290					295					300
Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
				305					310					315
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn
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Gly	Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val
				335					340					345
Ile	Asp	Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu
				350					355					360
Val	Thr	Glu	Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val
				365					370					375
Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser
				380					385					390
Asp	Gln	Trp	His	Val	Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys
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Gly	Gly	Pro	Ser	Thr	Pro	Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr
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<210> 277
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 <212> PRT
 <213> Homo sapiens
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Pro	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly		5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr		20	25	30
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr		35	40	45
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly		50	55	60
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr		65	70	75
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln		80	85	90
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala		95	100	105
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn		110	115	120
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn		125	130	135
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala		140	145	150
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser		155	160	165
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro		170	175	180
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser		185	190	195
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg		200	205	210
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg		215	220	225
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr		230	235	240
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp		245	250	255
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys		260	265	270
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr		275	280	285
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

290	295	300
Ile Asn Val Ile Arg His Ala Val Leu	Leu Pro Ala Asp Ser Pro	
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Leu Ala Pro His Ile Tyr Ala Val Phe	Thr Ser Gln Trp Gln Val	
320	325	330
Gly Gly Thr Arg Ser Ser Ala Val Cys	Ala Phe Ser Leu Leu Asp	
335	340	345
Ile Glu Arg Val Phe Lys Gly Lys Tyr	Lys Glu Leu Asn Lys Glu	
350	355	360
Thr Ser Arg Trp Thr Thr Tyr Arg Gly	Pro Glu Thr Asn Pro Arg	
365	370	375
Pro Gly Ser Cys Ser Val Gly Pro Ser	Ser Asp Lys Ala Leu Thr	
380	385	390
Phe Met Lys Asp His Phe Leu Met Asp	Glu Gln Val Val Gly Thr	
395	400	405
Pro Leu Leu Val Lys Ser Gly Val Glu	Tyr Thr Arg Leu Ala Val	
410	415	420
Glu Thr Ala Gln Gly Leu Asp Gly His	Ser His Leu Val Met Tyr	
425	430	435
Leu Gly Thr Thr Thr Gly Ser Leu His	Lys Ala Val Val Ser Gly	
440	445	450
Asp Ser Ser Ala His Leu Val Glu Glu	Ile Gln Leu Phe Pro Asp	
455	460	465
Pro Glu Pro Val Arg Asn Leu Gln Leu	Ala Pro Thr Gln Gly Ala	
470	475	480
Val Phe Val Gly Phe Ser Gly Gly Val	Trp Arg Val Pro Arg Ala	
485	490	495
Asn Cys Ser Val Tyr Glu Ser Cys Val	Asp Cys Val Leu Ala Arg	
500	505	510
Asp Pro His Cys Ala Trp Asp Pro Glu	Ser Arg Thr Cys Cys Leu	
515	520	525
Leu Ser Ala Pro Asn Leu Asn Ser Trp	Lys Gln Asp Met Glu Arg	
530	535	540
Gly Asn Pro Glu Trp Ala Cys Ala Ser	Gly Pro Met Ser Arg Ser	
545	550	555
Leu Arg Pro Gln Ser Arg Pro Gln Ile	Ile Lys Glu Val Leu Ala	
560	565	570
Val Pro Asn Ser Ile Leu Glu Leu Pro	Cys Pro His Leu Ser Ala	
575	580	585

Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
			590					595					600
Asp	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Gln
			605						610				615
Arg	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn
			620						625				630
Ile	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp
			635						640				645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu
			650						655				660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu
			665						670				675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val
			680						685				690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala
			695						700				705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys
			710						715				720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln
			725						730				735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val
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Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala			
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<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 278

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<210> 279

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<212> DNA

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<223> Synthetic construct.

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<212> Artificial

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<223> Synthetic construct.

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<210> 281
<211> 2320
<212> DNA
<213> Homo sapiens

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1 sapiens

496-502

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			5					10					15
	Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Thr
					20				25				30
	Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ile
					35					40			45
	Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	Arg
					50					55			60
	Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Gln
					65					70			75
	Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Lys
					80					85			90
	Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly
					95					100			105
	Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Gln
					110					115			120
	Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Lys
					125					130			135
	Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Cys
					140					145			150
	Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Ile
					155					160			165
	Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro
					170					175			180
	Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Met
					185					190			195
	Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Ser
					200					205			210
	Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Ile
					215					220			225
	Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Leu
					230					235			240
	Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe
					245					250			255
	Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Gly
													Gly

	260		265		270									
Pro	Ala	Glu	Lys	Pro	Ile	Lys	Pro	Val	Pro	Gln	Asp	Leu	Glu	Asn
				275					280					285
Leu	Ile	Ala	Lys	Phe	Gly	Asp	Ser	Gly	Phe	Val	Leu	Val	Thr	Leu
				290					295					300
Leu	Ser	Met	Val	Asn	Thr	Cys	Gln	Asn	Pro	Glu	Ile	Phe	Lys	Glu
				305					310					315
Met	Asn	Asn	Ala	Phe	Ala	His	Leu	Pro	Gln	Gly	Val	Ile	Trp	Lys
				320					325					330
Cys	Gln	Cys	Ser	His	Trp	Pro	Lys	Asp	Val	His	Leu	Ala	Ala	Asn
				335					340					345
Val	Lys	Ile	Val	Asp	Trp	Leu	Pro	Gln	Ser	Asp	Leu	Leu	Ala	His
				350					355					360
Pro	Ser	Ile	Arg	Leu	Phe	Val	Thr	His	Gly	Gly	Gln	Asn	Ser	Ile
				365					370					375
Met	Glu	Ala	Ile	Gln	His	Gly	Val	Pro	Met	Val	Gly	Ile	Pro	Leu
				380					385					390
Phe	Gly	Asp	Gln	Pro	Glu	Asn	Met	Val	Arg	Val	Glu	Ala	Lys	Lys
				395					400					405
Phe	Gly	Val	Ser	Ile	Gln	Leu	Lys	Lys	Leu	Lys	Ala	Glu	Thr	Leu
				410					415					420
Ala	Leu	Lys	Met	Lys	Gln	Ile	Met	Glu	Asp	Lys	Arg	Tyr	Lys	Ser
				425					430					435
Ala	Ala	Val	Ala	Ala	Ser	Val	Ile	Leu	Arg	Ser	His	Pro	Leu	Ser
				440					445					450
Pro	Thr	Gln	Arg	Leu	Val	Gly	Trp	Ile	Asp	His	Val	Leu	Gln	Thr
				455					460					465
Gly	Gly	Ala	Thr	His	Leu	Lys	Pro	Tyr	Val	Phe	Gln	Gln	Pro	Trp
				470					475					480
His	Glu	Gln	Tyr	Leu	Phe	Asp	Val	Phe	Val	Phe	Leu	Leu	Gly	Leu
				485					490					495
Thr	Leu	Gly	Thr	Leu	Trp	Leu	Cys	Gly	Lys	Leu	Leu	Gly	Met	Ala
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Val	Trp	Trp	Leu	Arg	Gly	Ala	Arg	Lys	Val	Lys	Glu	Thr		
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<210> 283
 <211> 24
 <212> DNA
 <213> Artificial

<210> Artificial Sequence
<211> 1-24
<213> Synthetic construct.

<400> 283
tggtttggt caccatcccc aagg 24

<210> 284
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 284
tcaggcttgt ctccaaagag aagg 24

<210> 285
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 285
cccaaagatg tccacctggc tgcaaatgtg aaaattgtgg actgg 45

<210> 286
<211> 2340
<212> DNA
<213> Homo sapiens

<400> 286
gggtgtgtga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50
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ccgttcacac acacatacca tgttctecat cccccaggt ccagccctca 150
gtgtgtgccc atccagcagg gctaccctga agctctgggt gcagccctcc 200
cgtccagtgg gcaggcgggt tcatccctcc ttctctctcc aaagcccaac 250
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gttcagcgag cctagagagg gcagactatc aggggtgccgg cggtgagaat 400
ccagggagag gaggcgaaac agaagagggg cagaagaccg gggcacttgt 450

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 ...agaggaactt aaatataaaa ctgtatacta aaattaaaaa 2340

<210> 287
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 287

Met	Leu	Gly	Ala	Lys	Pro	His	Trp	Leu	Pro	Gly	Pro	Leu	His	Ser
1				5					10					15
Pro	Gly	Leu	Pro	Leu	Val	Leu	Val	Leu	Leu	Ala	Leu	Gly	Ala	Gly
				20					25					30
Trp	Ala	Gln	Glu	Gly	Ser	Glu	Pro	Val	Leu	Leu	Glu	Gly	Glu	Cys
				35					40					45
Leu	Val	Val	Cys	Glu	Pro	Gly	Arg	Ala	Ala	Ala	Gly	Gly	Pro	Gly
				50					55					60
Gly	Ala	Ala	Leu	Gly	Glu	Ala	Pro	Pro	Gly	Arg	Val	Ala	Phe	Ala
				65					70					75
Ala	Val	Arg	Ser	His	His	His	Glu	Pro	Ala	Gly	Glu	Thr	Gly	Asn
				80					85					90
Gly	Thr	Ser	Gly	Ala	Ile	Tyr	Phe	Asp	Gln	Val	Leu	Val	Asn	Glu
				95					100					105
Gly	Gly	Gly	Phe	Asp	Arg	Ala	Ser	Gly	Ser	Phe	Val	Ala	Pro	Val
				110					115					120
Arg	Gly	Val	Tyr	Ser	Phe	Arg	Phe	His	Val	Val	Lys	Val	Tyr	Asn
				125					130					135
Arg	Gln	Thr	Val	Gln	Val	Ser	Leu	Met	Leu	Asn	Thr	Trp	Pro	Val
				140					145					150
Ile	Ser	Ala	Phe	Ala	Asn	Asp	Pro	Asp	Val	Thr	Arg	Glu	Ala	Ala
				155					160					165
Thr	Ser	Ser	Val	Leu	Leu	Pro	Leu	Asp	Pro	Gly	Asp	Arg	Val	Ser

	170	175	180
1	Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser		
	185	190	195

	Ser phe Ser Gly Phe Leu Ile Phe Pro Leu
	200 205

<10> 288

<11> 24

<12> DNA

<13> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 288

aggcagccac cagctctgtg ctac 24

<210> 289

<211> 27

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-27

<223> Synthetic construct.

<400> 289

cagagaggga agatgaggaa gccagag 27

<210> 290

<211> 42

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-42

<223> Synthetic construct.

<400> 290

ctgtgctact gcccttggac cctggggacc gagtgtctct gc 42

<210> 291

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 291

gtgttttctc tcgcgccacc actggccgcc ggcgcagct ccaggtgtcc 50

taqccgccca gcctcgaagc cgtcccgga cccctgtgct ctgcgcuaag 100

ccctgcgcc gccggccggg gcctgggcca ggggcgcggg gtgaagcggc 150

atggggg accgtgactg ggggggcttc aggcataag accctcatag 200
 gctcgcctc cgggggtcctg cggggcgagc gtcagcccg ggtgaccgg 250
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 aaaaaaaaaa aaaaaaaaaa 1570

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Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Glu Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 293

gctgacctgg ttcccatcta ctcc 24

<210> 294

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 294

cccacagaca cccatgacac ttcc 24

<210> 295

<211> 50

<212> DNA

<213> Artificial

<220>

1. Artificial Sequence
1-50
2. Synthetic construct.

1 295
aaqaalgaat tglacaaagc aggtgatctt cgaqaaagggc tccatggggcc 50

<210> 296
<211> 3060
<212> DNA
<213> Homo sapiens

<400> 296
gggcgggggg atggggggcg gggggggggg ggggggcaact cgcagagggc 50
ccgacgcagg gccggggcgg gccacgggccc gaqqaagcgcg gcggccagag 100
cggggcccgcg gaggcgacgc cgggggacccc cgcgcgaaga gcaggtggcg 150
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200
ggctctgctg accttgtgcc ttggaaggct gtccctcagcg agggggccgtg 250
caccgcctcc tgacgagcgc catgggcccg ctggcccttc tgaagaccca 300
gttcgtgctg cacctgctgg tcggctttgt ctccgtggcg agtggctctg 350
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cagctctacc gccgcctcaa ctgcgcctc gccactcac tctggagcca 450
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 accctgtctc 3060

<210> 297

<211> 368

<212> PRT

<213> Homo sapiens

<400> 297

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Leu	Val	Gly	Phe	Val	Phe	Val	Val	Ser	Gly	Leu	Val	Ile	Asn	Phe	20	25	30	
Val	Gln	Leu	Cys	Thr	Leu	Ala	Leu	Trp	Pro	Val	Ser	Lys	Gln	Leu	35	40	45	
Tyr	Arg	Arg	Leu	Asn	Cys	Arg	Leu	Ala	Tyr	Ser	Leu	Trp	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Cys	Thr	Glu	Cys	Thr	Leu	65	70	75	
Phe	Thr	Asp	Gln	Ala	Thr	Val	Glu	Arg	Phe	Gly	Lys	Glu	His	Ala	80	85	90	
Val	Ile	Ile	Leu	Asn	His	Asn	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Thr	Met	Cys	Glu	Arg	Phe	Gly	Val	Leu	Gly	Ser	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Leu	Tyr	Val	Pro	Leu	Ile	Gly	Trp	Thr	125	130	135	
Trp	Tyr	Phe	Leu	Glu	Ile	Val	Phe	Cys	Lys	Arg	Lys	Trp	Glu	Glu	140	145	150	
Asp	Arg	Asp	Thr	Val	Val	Glu	Gly	Leu	Arg	Arg	Leu	Ser	Asp	Tyr	155	160	165	

Ile	Glu	Tyr	Met	Trp	Phe	Leu	Leu	Tyr	Cys	Glu	Gly	Thr	Arg	Phe	
				170					175					180	
Thr	Glu	Thr	Lys	His	Arg	Val	Ser	Met	Glu	Val	Ala	Ala	Ala	Lys	
				185					190					195	
Gly	Leu	Pro	Val	Leu	Lys	Tyr	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	
				200					205					210	
Phe	Thr	Thr	Ala	Val	Lys	Cys	Leu	Arg	Gly	Thr	Val	Ala	Ala	Val	
				215					220					225	
Tyr	Asp	Val	Thr	Leu	Asn	Phe	Arg	Gly	Asn	Lys	Asn	Pro	Ser	Leu	
				230					235					240	
Leu	Gly	Ile	Leu	Tyr	Gly	Lys	Lys	Tyr	Glu	Ala	Asp	Met	Cys	Val	
				245					250					255	
Arg	Arg	Phe	Pro	Leu	Glu	Asp	Ile	Pro	Leu	Asp	Glu	Lys	Glu	Ala	
				260					265					270	
Ala	Gln	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Leu	Gln	
				275					280					285	
Glu	Ile	Tyr	Asn	Gln	Lys	Gly	Met	Phe	Pro	Gly	Glu	Gln	Phe	Lys	
				290					295					300	
Pro	Ala	Arg	Arg	Pro	Trp	Thr	Leu	Leu	Asn	Phe	Leu	Ser	Trp	Ala	
				305					310					315	
Thr	Ile	Leu	Leu	Ser	Pro	Leu	Phe	Ser	Phe	Val	Leu	Gly	Val	Phe	
				320					325					330	
Ala	Ser	Gly	Ser	Pro	Leu	Leu	Ile	Leu	Thr	Phe	Leu	Gly	Phe	Val	
				335					340					345	
Gly	Ala	Ala	Ser	Phe	Gly	Val	Arg	Arg	Leu	Ile	Gly	Glu	Ser	Leu	
				350					355					360	
Glu	Pro	Gly	Arg	Trp	Arg	Leu	Gln								
				365											

<210> 298

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 298

cttctctctgt ggggtggacca tgtgt 24

<210> 299

<211> 21

<212> DNA

<21> Artificial

<21>

<21> Artificial Sequence

<21> 1-21

<22> Synthetic construct.

<400> 299

gctcctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgtataagaag gagctgctct acgtgcccci catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

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tgctctgggg cagccaccag gcatattcat ctttgttgtt gttttcttt 100

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tcagtttgct ttgtggggtt ggtggcaggc aggcgggtt acgcctgata 200

cggccctggg ttagaaggga agggaagata aacttttata caaatgggga 250

tagctggggt ctgagacctg ctccctcagt aaaattcctg ggaletgcct 300

ataccttctt ttctctaacc tggcatacce tgcttaaagc ctctcagggc 350

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<211> 143

<212> PRT

<213> Homo sapiens

<400> 302

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			20						25					30
Leu	Leu	Ile	Ser	Leu	Val	Gly	Lys	Gly	Leu	Ser	Leu	Ser	Cys	Gly
			35						40					45
Val	Gly	Gly	Arg	Gln	Ala	Gly	Leu	Arg	Leu	Ile	Arg	Pro	Trp	Val
			50						55					60
Arg	Arg	Glu	Gly	Lys	Ile	Asn	Phe	Tyr	Thr	Asn	Gly	Asp	Ser	Trp
			65						70					75
Gly	Leu	Arg	Pro	Ala	Ser	Ser	Val	Lys	Phe	Leu	Gly	Ser	Ala	Tyr
			80						85					90
Thr	Phe	Phe	Ser	Leu	Thr	Trp	His	Thr	Leu	Leu	Lys	Ala	Ser	Gln
			95						100					105
Gly	Phe	Ser	Leu	Phe	Leu	Gly	Ser	Lys	Tyr	Leu	Glu	Leu	Gln	Glu
			110						115					120
Pro	Ser	Trp	Ser	Gly	Pro	Cys	Pro	Pro	Gly	Gln	Leu	His	Cys	Thr
			125						130					135
Cys	Gly	Val	Leu	Leu	Ser	Phe	Leu							

203
 1768
 DNA
 Homo sapiens

303

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 35 40 45
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly
 50 55 60
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro
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 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala
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 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly
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Arg Arg Arg Asp

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 <212> DNA
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<400> 305

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<211> 262

<212> PRT

<213> Homo sapiens

<400> 306

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			20						25				30	
Leu	Gly	Arg	Arg	Cys	Pro	Pro	Trp	Arg	Gly	Arg	Arg	Glu	Gln	Cys
			35						40				45	
Leu	Leu	Pro	Pro	Glu	Asp	Ser	Arg	Leu	Trp	Gln	Tyr	Leu	Leu	Ser
			50						55				60	

Arg Leu Leu
75

Cys Glu Gln
90

Ala Lys Lys
105

Leu Ala Leu
120

Cys Glu Val
135

Arg Gln Ala
150

Ala Leu Glu
165

Thr Phe Asp
180

Ala Tyr Tyr
195

Leu Ala Val
210

Pro Lys Gly
225

Arg Ile Arg
240

Gly Asp Gly
255

ctgggc 50

ctgttc 100

catcgc 150

cttttg 200

taacgac 250

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 a a g g c t g g g a t g g a g a a g g a g a a g g c c g a g g a g a a d c t g g c c g g g g a g g a 1800
 a t t t e c c g g g g a g g a g g c c c c a a g a q a a g g c g a g g a c a a g c c c a g c a 1850
 c a g g t c t c t a g c c c c a g t g a a t g g c g a g g c c a c a t c a c a g a a g g g g g a g 1900
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 a a g g t g t g g c t c t c t g a a g a c t g c a c g a g c g t a c g g g a g g g t c c c g 2000
 a c t g g a c a g g c c t g g g a g c g a c c g g c a g g a g c g c a g a g g g c a c g g g g g 2050
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 35 40 45
 Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro
 50 55 60
 Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys
 65 70 75
 Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala
 80 85 90
 Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala
 95 100 105
 Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp
 110 115 120
 Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala
 125 130 135
 Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

	140	145	150
	Ser Gly Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser
	155	160	165
	Val Ser Lys Arg Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala
	170	175	180
	Thr Val Ser Pro Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu
	185	190	195
	Ser Glu Lys Thr Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala
	200	205	210
	Ala Val Arg Ala Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys
	215	220	225
	Lys Lys Ala Pro Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser
	230	235	240
	Asp Gly Ala Lys Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser
	245	250	255
	Ser Ser Ser Ser Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val
	260	265	270
	Lys Lys Pro Pro Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro
	275	280	285
	Lys Pro Arg Gly Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser
	290	295	300
	Ser Ser Ser Asp Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu
	305	310	315
	Trp Lys Arg Arg Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg
	320	325	330
	Arg Arg Arg Glu Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln
	335	340	345
	Glu Lys Glu Glu Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly
	350	355	360
	Glu Ala Glu Arg Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg
	365	370	375
	Glu Asp Asp Glu Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly
	380	385	390
	Arg Gly Pro Pro Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu
	395	400	405
	Glu Arg Glu Ala Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser
	410	415	420
	Thr Glu Pro Ala Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg
	425	430	435

Ile	Leu	Glu	Lys	Gln	Gln	Ala	Lys	Pro	Val	Lys	Val	Glu	Arg	Thr	
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Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met	Asp	Arg	Lys	Val	Glu	Lys	
				455					460					465	
Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu	Gln	Lys	Leu	His	Ser	
				470					475					480	
Glu	Phe	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro	Asp	Val	Lys	Arg	
				485					490					495	
Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln	Val	Thr	Ser	
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Gln	Phe	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu	Lys	Lys	
				515					520					525	
Phe	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala	Ala	
				530					535					540	
Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile	
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Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	
				560					565					570	
Ala	Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	
				575					580					585	
Pro	Gln	Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	
				590					595					600	
Pro	Val	Asn	Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	
				605					610					615	
Asp	Lys	Glu	His	Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	
				620					625					630	
Cys	Gly	Ser	Ser	Glu	Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	
				635					640					645	
Asp	Leu	Asp	Arg	Pro	Gly	Ser	Asp	Arg	Gln	Glu	Arg	Glu	Arg	Ala	
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 <211> 777
 <212> PRT
 <213> Homo sapiens

<400> 310
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 35 40 45
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro
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 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu
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 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

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				95					100					105
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala
				110					115					120
Gln	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu
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Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala
				140					145					150
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu
				155					160					165
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg
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Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met
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Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly
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Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His
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His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly
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Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro
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Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val
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Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp
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				320					325					330
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe
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Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr
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Ile	Lys	Arg	His	Ser	Val	Met	Tyr	Lys	Ser	Val	Tyr	Pro	Val	Ala	
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Ile Val Lys Leu Thr Leu Asn Val Ile Glu Asn Glu Gln Met Glu					
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Asn Thr Gln Arg Ala Glu His Glu Glu Gly Gln Val Lys Asp Leu					
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Leu Ala Glu Ser Arg Leu Arg Tyr Lys Asp Tyr Ile Gln Ile Leu					
	710		715		720
Ser Ser Pro Asn Phe Ser Leu Asp Gln Tyr Cys Glu Gln Met Trp					
	725		730		735
His Arg Glu Lys Arg Arg Gln Arg Asn Lys Gly Gly Pro Lys Trp					
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 <213> Artificial

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 <223> Synthetic construct.

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<210> 312
 <211> 24
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-24
 <223> Synthetic construct.

<400> 312
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<210> 313
 <211> 45
 <212> DNA
 <213> Artificial

<220>
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 <222> 1-45
 <223> Synthetic construct.

<400> 313

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<210> 314

<211> 3934

<212> DNA

<213> Homo sapiens

<400> 314

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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

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Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala	
				35					40					45	
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg	
				50					55					60	
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu	
				65					70					75	
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala	
				80					85					90	
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser	
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Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp	
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Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu	
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Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro	
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Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp	
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Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu	
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Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu	
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Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser	
				200					205					210	
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu	
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Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln	
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Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly	
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Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu	
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Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu	
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Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala	

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111	Val Ser Val Leu Asp Gly Pro Pro Ala Pro Val Leu Pro Gly				
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	Asp Lys Ala Leu Asp Phe Pro Gly Phe Leu Asp Met Met Ala Pro				
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu
 50 55 60
 Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser
 65 70 75
 Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu
 80 85 90
 Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu
 95 100 105
 Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly
 110 115 120
 Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp
 125 130 135
 Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

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Arg Lys Ser Pro Ala Ser Gly	185	Gln Gly Pro Met Cys	190	Asn	195
Val Ala Pro Leu Gly Ser Pro Ser	200	Pro Arg Pro Arg Arg	205	Ala	210
Lys Arg Phe Ala Ser Leu Ser Arg Phe	215	Val Glu Thr Leu Val	220	Val	225
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Tyr Leu Leu Thr Val Met Ala Ala Ala	245	Ala Lys Ala Phe Lys	250	His	255
Pro Ser Ile Arg Asn Pro Val Ser Leu	260	Val Val Thr Arg Leu	265	Val	270
Ile Leu Gly Ser Gly Glu Glu Gly Pro	275	Gln Val Gly Pro Ser	280	Ala	285
Ala Gln Thr Leu Arg Ser Phe Cys Ala	290	Trp Gln Arg Gly Leu	295	Asn	300
Thr Pro Glu Asp Ser Gly Pro Asp His	305	Phe Asp Thr Ala Ile	310	Leu	315
Phe Thr Arg Gln Asp Leu Cys Gly Val	320	Ser Thr Cys Asp Thr	325	Leu	330
Gly Met Ala Asp Val Gly Thr Val Cys	335	Asp Pro Ala Arg Ser	340	Cys	345
Ala Ile Val Glu Asp Asp Gly Leu Gln	350	Ser Ala Phe Thr Ala	355	Ala	360
His Glu Leu Gly His Val Phe Asn Met	365	Leu His Asp Asn Ser	370	Lys	375
Pro Cys Ile Ser Leu Asn Gly Pro Leu	380	Ser Thr Ser Arg His	385	Val	390
Met Ala Pro Val Met Ala His Val Asp	395	Pro Glu Glu Pro Trp	400	Ser	405
Pro Cys Ser Ala Arg Phe Ile Thr Asp	410	Phe Leu Asp Asn Gly	415	Tyr	420
Gly His Cys Leu Leu Asp Lys Pro Glu	425	Ala Pro Leu His Leu	430	Pro	435

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455	Ile	Ile	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	465
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620	Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	630
635	Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	645
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680	Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	690
695	Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	705
710	Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	720
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Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr					
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	770		775		780
Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg					
	785		790		795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro					
	800		805		810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu					
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<210> 319
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 <213> Artificial

<220>
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 <223> Synthetic construct.

<400> 319
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<210> 320
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211 221
1197
212 JNA
213 Homo sapiens

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<210> 322

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 19 Homo sapiens

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 22 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys
 20 25 30
 23 Ile Cys Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val
 35 40 45
 24 Leu Phe Trp Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys
 50 55 60
 25 Ala Tyr Asp Met Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys
 65 70 75
 26 Lys Ile Tyr Met Glu Ile Asp Pro Val Thr Arg Thr Glu Ile Phe
 80 85 90
 27 Arg Ser Gly Asn Gly Thr Asp Glu Thr Leu Glu Val His Asp Phe
 95 100 105
 28 Lys Asn Gly Tyr Thr Gly Ile Tyr Phe Val Gly Leu Gln Lys Cys
 110 115 120
 29 Phe Ile Lys Thr Gln Ile Lys Val Ile Pro Glu Phe Ser Glu Pro
 125 130 135
 30 Glu Glu Glu Ile Asp Glu Asn Glu Glu Ile Thr Thr Thr Phe Phe
 140 145 150
 31 Glu Gln Ser Val Ile Trp Val Pro Ala Glu Lys Pro Ile Glu Asn
 155 160 165
 32 Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu Ile Cys Asp Asn
 170 175 180
 33 Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser Val Ser Glu
 185 190 195
 34 Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe Pro Ala
 200 205 210
 35 Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val Pro
 215 220 225
 36 Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
 230 235 240
 37 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe
 245 250 255
 38 Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg
 260 265 270

Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
275 280 285

Tyr Pro Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
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Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly
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Arg Val

<210> 323

<211> 1174

<212> DNA

<213> Homo sapiens

<400> 323

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 1097 tttat gaaaaaaaaa aaaa 1174

211 24
 211 239
 211 PRT
 211 Homo sapiens

1098 24
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 Tyr Leu Lys Gly Leu Trp Met Glu Cys Val Trp His Ser Thr Gly
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 65 70 75
 Asp Leu Gln Ala Ala Arg Ala Leu Met Val Ile Ser Cys Leu Leu
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 Arg Cys Ala Lys Gly Thr Pro Ala Lys Thr Thr Phe Ala Ile Leu
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 155 160 165
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 185 190 195
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 <213> Homo sapiens

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<210> 326

<211> 261

<212> PRT

<213> Homo sapiens

<400> 326

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				20					25					30
Ser	Thr	Gln	Asp	Leu	Tyr	Asp	Asn	Pro	Val	Thr	Ser	Val	Phe	Gln
				35					40					45
Tyr	Glu	Gly	Leu	Trp	Arg	Ser	Cys	Val	Arg	Gln	Ser	Ser	Gly	Phe
				50					55					60
Thr	Glu	Cys	Arg	Pro	Tyr	Phe	Thr	Ile	Leu	Gly	Leu	Pro	Ala	Met
				65					70					75
Leu	Gln	Ala	Val	Arg	Ala	Leu	Met	Ile	Val	Gly	Ile	Val	Leu	Gly

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Ala	Ile Gly Leu	Leu Val Ser Ile Phe	Ala Leu Lys Cys Ile Arg		
	95		100		105
Ile Gly Ser Met	Glu Asp Ser Ala Lys	Ala Asn Met Thr Leu Thr			
	110		115		120
Ile Gly Ile Met	Phe Ile Val Ser Gly	Leu Cys Ala Ile Ala Gly			
	125		130		135
Val Ser Val Phe	Ala Asn Met Leu Val	Thr Asn Phe Trp Met Ser			
	140		145		150
Thr Ala Asn Met	Tyr Thr Gly Met Gly	Gly Met Val Gln Thr Val			
	155		160		165
Gln Thr Arg Tyr	Thr Phe Gly Ala Ala	Leu Phe Val Gly Trp Val			
	170		175		180
Ala Gly Gly Leu	Thr Leu Ile Gly Gly	Val Met Met Cys Ile Ala			
	185		190		195
Cys Arg Gly Leu	Ala Pro Glu Glu Thr	Asn Tyr Lys Ala Val Ser			
	200		205		210
Tyr His Ala Ser	Gly His Ser Val Ala	Tyr Lys Pro Gly Gly Phe			
	215		220		225
Lys Ala Ser Thr	Gly Phe Gly Ser Asn	Thr Lys Asn Lys Lys Ile			
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 <212> DNA
 <213> Homo sapiens

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 gtgggcacag tggctgtcac tgtcatgctt cagtggagag tgtcggcctt 200
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250
 tgaattgcgt gaggcaggct aacatcagga tgcagtgc aaatctatgat 300
 tccctgctgg ctcttctctc ggacctacag gcagccagag gactgatgtg 350

tcttgcttcc gtagatgctt tcttggcttt catgatggcc atccttggca 400
 tgaatgcac caggtgcacg ggggacaatg agaaggtdaa ggcacacatt 450
 ctgtgaagg ctggaatcat ctccatcatc acgggcatgg tgggtgcctat 500
 ccttgtgagc tgggttggca atgccatcat cagagatttc tataactcaa 550
 taqtgaatgt tgcacaaaaa cgtgagcttg gagaagctct ctacttagga 600
 tggaccacgg cactggtgct gattgttggg ggagctctgt tctgtcgcgt 650
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 atgcacacac ccaaaaaagt tatcacaccg gaaagaagtc accgagcgtc 750
 tactccagaa gtcagtatgt gtagtttgtt atgttttttt aactttacta 800
 taaagccatg caaatgacaa aaatctatat tactttctca aaatggacc 850
 caaagaaact ttgatttact gttcttaact gcctaactct aattacagga 900
 actgtgcctc agctatttat gattctataa gctatttcag cagaatgaga 950
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 taaggtgggt caagcatcta ctctttttat catttacttc aaaatgacat 1050
 tgctaaagac tgcattttt tactactgta atttctccac gacatagcat 1100
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 actcaactat tgcctttcag ggaatcatg gatagggttg aagaaggtta 1250
 ctattaattg tttaaaaaca gcttagggat taatgtcttc catttataat 1300
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 gagtacagac tttgaggttt catcaatata aataaaagag cagaaaaata 1700
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atttttgttgc tctgaaaaat aaatttcctt cttgtaccat tttgttttaq 1850
 ttttactaaa atctgtaaat actgtatttt tctgtttatt ccaaatttga 1900
 ttttctgac aatccaattt gaaagtttgt gtcgacgtct gtcctagctta 1950
 attgaaatgtg ttctatttgc ttatacatt tatattaata aattgtacat 2000
 ttttctaatt 2010

<210> 328
 <211> 225
 <212> PRT
 <213> Homo sapiens

<400> 328
 Met Ala Thr His Ala Leu Glu Ile Ala Gly Leu Phe Leu Gly Gly
 1 5 10 15
 Val Gly Met Val Gly Thr Val Ala Val Thr Val Met Pro Gln Trp
 20 25 30
 Arg Val Ser Ala Phe Ile Glu Asn Asn Ile Val Val Phe Glu Asn
 35 40 45
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile
 50 55 60
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro
 65 70 75
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met
 80 85 90
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr
 95 100 105
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu
 110 115 120
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile
 125 130 135
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn
 140 145 150
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu
 155 160 165
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala
 170 175 180
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr
 185 190 195
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His
 200 205 210

Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329
 <211> 1315
 <212> DNA
 <213> Homo sapiens

<400> 329
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 gaccgcttcc atcggaaca gcctcgtggt gcccaggtg gtgtgggagg 150
 gccgtgggat gtctgcgtg gtgcagagca ccggccagat gcagtgcagg 200
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250
 cctctgtgtc atgcccctcc ttgtggccct gttcggcttg ctggtctacc 300
 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaagcc 350
 cgcttggtgc tcacctctgg gattgtcttt gtcctctcag gggctctgac 400
 gctaattccc gtgtgctgga cggcgcatgc catcatccgg gacttctata 450
 accccctggt ggctgaggcc caaaagcggg agctgggggc ctccctctac 500
 ttgggctggg cggcctcagg cttttgttg ctgggtgggg ggltgctgtg 550
 ctgcacttgc cctcggggg ggtcccaggg cccagccat tacatggccc 600
 gctactcaac atctgccct gccatctctc gggggccctc tgagtacct 650
 accaagaatt acgtctgagc tggaggggaa tgggggctcc gctggcgcta 700
 gagccatcca gaagtggcag tgcacaacag ctttgggatg ggttcgtacc 750
 ttttgtttct gctcctgct atttttcttt tgactgagga tattaaaaat 800
 tcatttgaaa actgagccaa ggtgttgact cagactctca cttaggctct 850
 gctgtttctc accttggat gatggagcca aagaggggat gctttgagat 900
 tctggatctt gacatgccca tcttgaagc cagtcaagct atggaactaa 950
 tgaggaggct gcttgctgtg ctggcttttc aacaagacag actgtcccca 1000
 agagttcctg ctgctgctgg gggctgggct tccctagatg tcaactggaca 1050
 gctgcccccc atctactca ggtctctgga gctcctctct tcaccttg 1100
 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150
 cctctgttcc ctccgtctg ataagacgic cccccccag ggccaggtcc 1200
 cagctatgta gacccccgc cccacctcna acactgcacc cttctgcct 1250

gccccctcg tctcaccccc tttaacttca catttttata aaataaaqca 1300

tttttgita gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

Met Ala Ser Ala Gly Met Gln Ile Leu Gly Val Val Leu Thr Leu
1 5 10 15

Leu Gly Trp Val Asn Gly Leu Val Ser Cys Ala Leu Pro Met Trp
20 25 30

Lys Val Thr Ala Phe Ile Gly Asn Ser Ile Val Val Ala Gln Val
35 40 45

Val Trp Glu Gly Leu Trp Met Ser Cys Val Val Gln Ser Thr Gly
50 55 60

Gln Met Gln Cys Lys Val Tyr Asp Ser Leu Leu Ala Leu Pro Gln
65 70 75

Asp Leu Gln Ala Ala Arg Ala Leu Cys Val Ile Ala Leu Leu Val
80 85 90

Ala Leu Phe Gly Leu Leu Val Tyr Leu Ala Gly Ala Lys Cys Thr
95 100 105

Thr Cys Val Glu Glu Lys Asp Ser Lys Ala Arg Leu Val Leu Thr
110 115 120

Ser Gly Ile Val Phe Val Ile Ser Gly Val Leu Thr Leu Ile Pro
125 130 135

Val Cys Trp Thr Ala His Ala Ile Ile Arg Asp Phe Tyr Asn Pro
140 145 150

Leu Val Ala Glu Ala Gln Lys Arg Glu Leu Gly Ala Ser Leu Tyr
155 160 165

Leu Gly Trp Ala Ala Ser Gly Leu Leu Leu Leu Gly Gly Gly Leu
170 175 180

Leu Cys Cys Thr Cys Pro Ser Gly Gly Ser Gln Gly Pro Ser His
185 190 195

Tyr Met Ala Arg Tyr Ser Thr Ser Ala Pro Ala Ile Ser Arg Gly
200 205 210

Pro Ser Glu Tyr Pro Thr Lys Asn Tyr Val
215 220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

331
ccccaaaggaga acatcatcaca agactttctct agactcaaaa ggtttccacg 50
tttaccatct tgagcatctt ctaccactcc gaattgaacc agtcttccaaa 100
gttaaaaggcaa tggcatttta tcccttgcaa attgctgggc tggttcttg 150
gttcccttggc atggttggga ctcttccac aacctttctg cctcagtggt 200
taagtatcag cttttgttgg cagcaacatt attgtctttg agaggtctg 250
ggaagggtct tggatgaatt gcatccgaca agccagggtc cggttgcaat 300
gcaagttcta tagctcttg ttggtctcc cgcctgccct ggaacagcc 350
cgggcccctca tgtgtgtggc tgttctctc tcttgatcg cctgtctat 400
tggcatctgt ggcataaagc aggtccagt caccaggtct aacgagaggg 450
ccaaagcata ccttctggga acttcaggag tctcttctat cctgacgggt 500
atcttcgttc tgattccggt gagctggaca gccaatataa tcatcagaga 550
tttctacaac ccagccatcc acataggcca gaaacgagag ctgggagcag 600
cacttttctt tggctgggca agcgtctgt tctcttctat tggagggggg 650
ctgctttgtg gattttgtg ctgcaacaga aagaagcaag ggtacagata 700
tccagtgcct ggctaccgtg tgccacacac agataagcga agaaatacga 750
caatgcttag taagacctcc accagttatg tataatgcct ccttttgggt 800
ccaagtatgg acataggtca atgttttcta taaagtctg ctgaaaactg 850
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900
cgaaagtctc aatttcttac tgggtgtagg aatgaaaatg acttacttgg 950
acattctgac ttcagggtga ttaaagcat tgactattgt tggacccaat 1000
cgctgctcca attttcatat tctaaattca agtatacca taatcattag 1050
caagtgtaca atgatggact acttattact ttttgaccat catgtattat 1100
ctgataagaa tctaaagttg aaattgatat tctataacaa taaaacatat 1150
acctattcta 1160

<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

	5	10	15
1	Ser Ser Leu Leu Ala Leu Pro Pro Ala Leu Glu Thr Ala Arg		
	20	25	30
2	Ala Leu Met Cys Val Ala Val Ala Leu Ser Leu Ile Ala Leu Leu		
	35	40	45
3	Ile Gly Ile Cys Gly Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
	50	55	60
4	Glu Arg Ala Lys Ala Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
	65	70	75
5	Ile Leu Thr Gly Ile Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
	80	85	90
6	Asn Ile Ile Ile Arg Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
	95	100	105
7	Gln Lys Arg Glu Leu Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
	110	115	120
8	Ala Ala Val Leu Phe Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
	125	130	135
9	Cys Cys Asn Arg Lys Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
	140	145	150
10	Tyr Arg Val Pro His Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
	155	160	165
11	Ser Lys Thr Ser Thr Ser Tyr Val		
	170		

<210> 333
 <211> 535
 <212> DNA
 <213> Homo sapiens

<400> 333
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 ctcagaagct gctagtctgt ctccaaaaaa agtggactgc aqcattttaca 150
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350
 tcatcatccc aggcctctgac tgagtttctt tcagttttac tgatgttctg 400
 ggtgqgggac agagccagat tcagagtaat cttgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr
1 5 10 15

Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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tggccctgac cgggctggcg ctgctcctgc tctgtgtctg gggcccaggt 150

ggcataagtg gaaataaaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaaag tggccgttga tgagaataaa gccaaagaat 250

tccctggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccgaggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaattt gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattggtc cccggagccc ctacggcttt aggcatggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaaatt 550

agcgattctc ttcattgtatc tccaatgccc tiacactact tggttttctga 600

tttctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650
 gtttggttaa aacaacacat qtaaatgcct tttgataatt catgggaatg 700
 tttt aaaaatagaa ataaagcatt ttgtaaaaa ga 742

<336>
 <148>
 FRT
 Homo sapiens

<400> 336
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly
 1 5 10 15
 Leu Ala Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser
 20 25 30
 Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val
 35 40 45
 Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu
 50 55 60
 Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg
 65 70 75
 Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met
 80 85 90
 Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu
 95 100 105
 Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln
 110 115 120
 Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr
 125 130 135
 Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr
 140 145

<210> 337
 <211> 1310
 <212> DNA
 <213> Homo sapiens

<400> 337
 cggctcgagc ccgcccggaa gtgcccgagg ggccgcgatg gagctggggg 50
 agccggggcgc tcggtagcgc ggcgggcaag gcaggcgcca tgacctgat 100
 tgaaggggtg ggtgatgagg tgaccgtcct tttctcggtg cttgectgcc 150
 ttctggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgaggggcggg 200
 gacccaactgc ccagccgtc agggacccca acgccatccc agcccagcgc 250

111 gggca gctaccgaca gcatgagagg ggaggcccca ggggcagaga 300
 112 agcct gagacacaga ggtcaagctg cacagccaga gcccaqcacg 350
 113 acag caacaccgcc agcccggac tcccgcagg agccctcgt 400
 114 aggtg aaattcctca atgattcaga gcagggtggc agggcctggc 450
 115 gacac cattggctcc ttgaaaagga cccagtttcc cggccgggaa 500
 116 aggtgac gactcatcta ccaagggcag ctgctaggcg acgacacca 550
 117 agc aggc agccttcacc tccctcccaa ctgcgttctc cactgccacg 600
 118 tctcagag agtcgggtccc ccaaattccc cctgcccgcc ggggtccgag 650
 119 cccgcccct ccgggtgga aatcggcagc ctgctgctgc cctgctgct 700
 120 cctgctgttg ctgctgctct ggtactgcca gatccagtac cggcccttct 750
 121 tcccctgac cgcactctg ggcttgccg gcttcacct gctcctcagt 800
 122 cctctggcct ttgccatgta ccgcccgtag tgccctcccg ggcgcttggc 850
 123 agcgtgccg gccctcccg accttgctcc ccgcgcccg gcgggagctg 900
 124 ctgctgccc aggcgccct ctccggcctg cctcttccc ctgccctgga 950
 125 gccagccct gcgcgcaga ggactcccg gactggcgga ggccccgcc 1000
 126 tgcgaccgcc ggggctcggg gccacctccc ggggtgctg aacctcagcc 1050
 127 cgcactggga gtgggtcct cggggtcggg catctgctgt cgtgcctcg 1100
 128 gccccgggca gagccgggc gccccgggg cccgtcttag tgttctgccg 1150
 129 gaggaccag ccgcctccaa tccctgacag ctccctgggc tgagttgggg 1200
 130 acgccaggtc ggtgggaggc tggggaagg gagcggggag gggcagagga 1250
 131 gttccccga acccgtgcag attaaagtaa ctgtgaagtt ttaaaaaaaaa 1300
 aaaaaaaaa 1310

<210> 338

<211> 246

<212> PRT

<213> Homo sapiens

<400> 338

Met	Thr	Leu	Ile	Glu	Gly	Val	Gly	Asp	Glu	Val	Thr	Val	Leu	Phe
1				5				10					15	
Ser	Val	Leu	Ala	Cys	Leu	Leu	Val	Leu	Ala	Leu	Ala	Trp	Val	Ser
			20					25					30	
Thr	His	Thr	Ala	Glu	Gly	Gly	Asp	Pro	Leu	Pro	Gln	Pro	Ser	Gly
			35					40					45	

Thr	Pro	Thr	Pro	Ser	Gln	Pro	Ser	Ala	Ala	Met	Ala	Ala	Thr	Asp	50	55	60
Leu	Met	Arg	Gly	Glu	Ala	Pro	Gly	Ala	Glu	Thr	Pro	Ser	Leu	Arg	65	70	75
Leu	Arg	Gly	Gln	Ala	Ala	Gln	Pro	Glu	Pro	Ser	Thr	Gly	Phe	Thr	80	85	90
Ala	Thr	Pro	Pro	Ala	Pro	Asp	Ser	Pro	Gln	Glu	Pro	Leu	Val	Leu	95	100	105
Arg	Leu	Lys	Phe	Leu	Asn	Asp	Ser	Glu	Gln	Val	Ala	Arg	Ala	Trp	110	115	120
Pro	His	Asp	Thr	Ile	Gly	Ser	Leu	Lys	Arg	Thr	Gln	Phe	Pro	Gly	125	130	135
Arg	Glu	Gln	Gln	Val	Arg	Leu	Ile	Tyr	Gln	Gly	Gln	Leu	Leu	Gly	140	145	150
Asp	Asp	Thr	Gln	Thr	Leu	Gly	Ser	Leu	His	Leu	Pro	Pro	Asn	Cys	155	160	165
Val	Leu	His	Cys	His	Val	Ser	Thr	Arg	Val	Gly	Pro	Pro	Asn	Pro	170	175	180
Pro	Cys	Pro	Pro	Gly	Ser	Glu	Pro	Gly	Pro	Ser	Gly	Leu	Glu	Ile	185	190	195
Gly	Ser	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	200	205	210
Trp	Tyr	Cys	Gln	Ile	Gln	Tyr	Arg	Pro	Phe	Phe	Pro	Leu	Thr	Ala	215	220	225
Thr	Leu	Gly	Leu	Ala	Gly	Phe	Thr	Leu	Leu	Leu	Ser	Leu	Leu	Ala	230	235	240
Phe	Ala	Met	Tyr	Arg	Pro										245		

<210> 339

<211> 849

<212> DNA

<213> Homo sapiens

<400> 339

gagattggaa acagccaggt tggagcagtg agtgagtaag gaaacctggc 50

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atgacaaaagg cgctactcat ctatttggtc agcagctttc ttgccctaaa 200

tcaggccagc ctcatcagtc gctgtgactt ggcccaggtg ctgcagctgg 250

tggga tgggtttgag gggtactccc tgagtgaactg gctgtgcctg 300
 gttttgtgg aaagcaagtt caacatatca aagataaatg aaaatgcgga 350
 tttttttt gactatggcc ttttccagat caacagccac tactggtgca 400
 ttttataa gagttactcg gaaaaccttt gccacgtaga ctgtcaagat 450
 tttgaatc ccaacctttct tgcaggcatc cactgcgcaa aaaggattgt 500
 gttgggagca cgggggatga acaactgggt agaattggagg ttgcactgtt 550
 cgggcgggcc actctcctac ttgctgacag gatgccgctt gagatgaaac 600
 aaggtgctggg tgcaccgtgg agtcattcca agactcctgt cctcactcag 650
 ggatttttca ttttttcttc ctactgcctc cacttcatgt tattttcttc 700
 ccttccattt tacaactaaa actgaccaga gccccaggaa taaatggttt 750
 tcttggtctc ctcttactc ccatctggac ccagtcacctt gggtcctgtc 800
 tgttatttgt aaactgagga ccacaataaa gaaatcttta tatttatcg 849

<210> 340

<211> 148

<212> PRT

<213> Homo sapiens

<400> 340

Met	Thr	Lys	Ala	Leu	Leu	Ile	Tyr	Leu	Val	Ser	Ser	Phe	Leu	Ala
1				5					10					15
Leu	Asn	Gln	Ala	Ser	Leu	Ile	Ser	Arg	Cys	Asp	Leu	Ala	Gln	Val
				20					25					30
Leu	Gln	Leu	Glu	Asp	Leu	Asp	Gly	Phe	Glu	Gly	Tyr	Ser	Leu	Ser
				35					40					45
Asp	Trp	Leu	Cys	Leu	Ala	Phe	Val	Glu	Ser	Lys	Phe	Asn	Ile	Ser
				50					55					60
Lys	Ile	Asn	Glu	Asn	Ala	Asp	Gly	Ser	Phe	Asp	Tyr	Gly	Leu	Phe
				65					70					75
Gln	Ile	Asn	Ser	His	Tyr	Trp	Cys	Asn	Asp	Tyr	Lys	Ser	Tyr	Ser
				80					85					90
Glu	Asn	Leu	Cys	His	Val	Asp	Cys	Gln	Asp	Leu	Leu	Asn	Pro	Asn
				95					100					105
Leu	Leu	Ala	Gly	Ile	His	Cys	Ala	Lys	Arg	Ile	Val	Ser	Gly	Ala
				110					115					120
Arg	Gly	Met	Asn	Asn	Trp	Val	Glu	Trp	Arg	Leu	His	Cys	Ser	Gly
				125					130					135
Arg	Pro	Leu	Ser	Tyr	Trp	Leu	Thr	Gly	Cys	Arg	Leu	Arg		

<210> 341
 <211> 23
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-23
 <223> Synthetic construct.

<400> 341
 ttttccaagg atgacaaagg cgc 23

<210> 342
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-29
 <223> Synthetic construct.

<400> 342
 ggtcagcagc ttctttgccc taaatcagg 29

<210> 343
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 343
 atctcaggcg gcatcctgtc agcc 24

<210> 344
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 344
 gtggatgcct gcaagaaggt tggg 24

<210> 345
 <211> 45
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-45
 <223> Synthetic construct.

<400> 345
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<210> 346
 <211> 2575
 <212> DNA
 <213> Homo sapiens

<400> 346
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 aaggagaaaa cggggglaaa gggaggggaag caattcaatt tgaagtcctt 200
 gtgaatgggc ttccagaagg caattaaaga aatccactca gagaggactt 250
 ggggtgaaac ttgggtcctg tggttttctg attgtaagtg gaagcaggtc 300
 ttgcacacgc tgttggcaaa tgcaggacc aggttaagtg actggcagaa 350
 aaacttccag gtggaacaag caaccatgt tctgctgcaa gcttgaagga 400
 gccctggagcg ggagaaagct aacttgaaca tgacctgttg catttgcaa 450
 gttctagcaa catgctccta aggaagcgat acaggcacag accatgcaga 500
 ctccagttcc tctgctgct cctgatgctg ggatgcgtcc tgatgatggt 550
 ggcgatgttg caacctcccc accacacct gcaccagact gtcacagccc 600
 aagccagcaa gcacagccct gaagccaggt accgcctgga ctttggggaa 650
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 tctggagggc ctgccacct ttatctcact ggggaggat cagctgctgg 750
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 agtgcctgca tccccctcca gagggtcttg cccgaggtgc ggcacctact 1000
 gtgtctgcag cagcaccctc aggacagcct gccacagcc agcgtcatcc 1050
 tctgtttcca tgatgaggcc tggctcactc tctgaggac tgtacacagc 1100

caa cagtgccacag ggcccttcctg aaggagatca tccctcgttga 1150
 ggc cagcaaggac aactcaagtc tgcctcagc gaataatgtg 1200
 gaa gggggtgaag ttactcagaa gcaacaagaq gctgggtgac 1250
 ggc ggatcctggg ggccaccaga gccaccgggg atgtgctcgt 1300
 ggc ggcacitgg agtgcacccc aggttggtg gagcccccctc 1350
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 ggc ggcacttt ccagtaatac ccccaaaagg acctgcagcg 1450
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 ggc ggcctccag tccccataa gccccatcag gagccctgtg 1550
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cttttcattg actgctggct gctta 2575

4210 347

4211 639

4212 PRT

4213 Homo sapiens

4400 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
1				5					10					15
Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30
Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45
Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60
Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75
Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90
Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105
Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120
Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135
Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150
Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165
Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180
Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195
Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210
Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225
Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240
Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

545	550	555
Val Ser Pro Gln His Leu Cys Phe Ala Val Arg Gln Glu Gln Val		
560	565	570
Ile Leu Gln Asn Cys Thr Glu Glu Gly Leu Ala Ile His Gln Gln		
575	580	585
Ile Trp Asp Phe Gln Glu Asn Gly Met Ile Val His Ile Leu Ser		
590	595	600
Gly Lys Cys Met Glu Ala Val Val Gln Glu Asn Asn Lys Asp Leu		
605	610	615
Tyr Leu Arg Pro Cys Asp Gly Lys Ala Arg Gln Gln Trp Arg Phe		
620	625	630
Asp Gln Ile Asn Ala Val Asp Glu Arg		
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<210> 348

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 348

ggagaggtgg tggccatgga cag 23

<210> 349

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 349

ctgtcactgc aaggagccaa cacc 24

<210> 350

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 350

tatgtcgtcg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351
 <211> 2524
 <212> DNA
 <213> Homo sapiens

<400> 351
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 ctacagacatg gagtcacagga tgtggcctgc gctgctgctg tcccacctcc 100
 tccctctctg gccactgctg ttgttgcccc tcccaccgcc tgcacagggc 150
 tcttcacctc cccctcgaa cccaccagcc ccagcccgcc ccccggtgtg 200
 cagggggaggg cctcgggcc cactgcatgt gtgctgtgtg gaggcagcac 250
 ctccaccaag ccgactcctc cgggcccaca gatcaggtcg gcaagtcctg 300
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 aggatggagg ggaccccaac tctgccaatc ccggatttct ggaactatgt 450
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 gcgaggtgat ggagatgggc ttatccttgg agaggcacct gccaccctgc 550
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 tcaaataaag cctttgcaag ataa 2524

<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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I	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala	
									25					30	
Se	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg	
				35					40					45	
Cle	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala	
				50					55					60	
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro	
				65					70					75	
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys	
				80					85					90	
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn	
				95					100					105	
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu	
				110					115					120	
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser	
				125					130					135	
Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	
				230					235					240	

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgggtcccg cccgccgctg cctcactcc 50

cggccaggat ggcatactgt ctggccctgc gcattggcgt gctgctggtc 100

tccggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150
 cgtgcccacg ctgtggaacg agccggccga gctgcccgcg ggagaaggcc 200
 ccctgagag caccagcccc ggccgggagc ccgtggacac cggccccca 250
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 tgcgcgccct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400
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 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354
 <211> 121
 <212> PRT
 <213> Homo sapiens

<400> 354
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 20 25 30
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly
 35 40 45
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp
 50 55 60
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser
 65 70 75
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro
 80 85 90
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys
 95 100 105
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala
 110 115 120

Ser

<210> 355
 <211> 2134
 <212> DNA
 <213> Homo sapiens

<400> 355
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 gttggccggc ggccggcccg gacgggcatg gccctgctgc tctgacctgt 100

gtgcctgaag ggggegetgg cccacggctg tctgcactgc cacagcaact 150
 tctccaaqaa gtltctcttc taccgcaacc atgtgaactt caagtctctg 200
 tgggtggggc acatccccgt gtcagggggc ctgctcaccg actggagcga 250
 cgacacgatg aaggagctgc acctggccat ccccgccaag atcaccggg 300
 agaagctgga ccaagtggcg acagcagtggt accagatgat ggatcagctg 350
 taccagggga agatgtactt ccccggtat tccccaacg agctgcgaaa 400
 catcttcggg gaggaggtgc acctcatcca gaacgccatc atcgaaaggc 450
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 tgcctcatct cacgtgggg gtcaacctgg ggacccttc cctcggggc 650
 atggacacac atacatgaaa accaggccgc atcgactgtc agcaccgctg 700
 tggcatcttc caqtacgaga ccattctctg caacaactgc acagactcgc 750
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 acccgtgcca gggccctact gtccctgggg tcccaggctc tcttggagg 850
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 tggaaqtcag ctgtccagg cctcctgaac tacataaata actggcaca 1000
 gtaagtcccc tctcaaacc aacacaggca gtgtgtgtat gtgagcaact 1050
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 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650
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 aacctgacct tggaagatgc tgctgaqtgt ctcaagcagc actgacagca 1900
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 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100
 ctgcgggatg tgattaaagt cctgatgtt tctc 2134

<210> 356
 <211> 157
 <212> PRT
 <213> Homo sapiens

<400> 356
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala
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 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser
 20 25 30
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp
 35 40 45
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr
 50 55 60
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu
 65 70 75
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln
 80 85 90
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu
 95 100 105
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala
 110 115 120
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln
 125 130 135
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro
155

<210> 357

<211> 1536

<212> DNA

<213> Homo sapiens

<400> 357

accagagaca ggagaggac aatggaagct gccccgtcca gggtcatgtt 50
 cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100
 ttgagaaatc ctcatatggt cctgggtgctg cccaggaacc cactgtggctc 150
 acagatgtcc caqctgccat ggaattcatt gctgccactg aggtggctgt 200
 cataggtctt ttccaggatt tagaaatacc agcagtgcc atactccata 250
 gcatgggtga aaaattccca ggctgtgcat ttgggatcag cactgattct 300
 gaggtttctga cacactacaa catcactggg aacaccatct gctctttctg 350
 cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400
 ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450
 gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500
 tcagattcat ctctctctga taatgaacaa ggctcccca gagtatgaag 550
 agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600
 ctctttatct tgggtggacg tgggatgaaa gaaaatggga aggtgatata 650
 atttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700
 ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750
 catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800
 aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850
 ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900
 aactcaaatc tcagagacac taaacaacag gatcactagg cctgcccaacc 950
 acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000
 gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050
 tctcttcttc cttcttttaa atttcatatc ctcaactcct atccaatttc 1100
 cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150
 tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctatagaag attgttccaa ttgtcattt aatatcaagt ttgtatactg 1250
 caaatgactt acacacaaca tagttcctgc tcttttaagg ttacctaaagg 1300
 ttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350
 tctaaaacca aaggatgggt ttaaacacct ttgtgaaatt gtccttttgc 1400
 ctgaagttaa aggtgtctc caagtcctg aactcagcag aaatagacca 1450
 tgtgaaaact ccattgttg ttagcatctc caactcccta tgtaaatcaa 1500
 caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358

<211> 273

<212> PRT

<213> Homo sapiens

<400> 358

Met	Glu	Ala	Ala	Pro	Ser	Arg	Phe	Met	Phe	Leu	Leu	Phe	Leu	Leu	1	5	10	15
Thr	Cys	Glu	Leu	Ala	Ala	Glu	Val	Ala	Ala	Glu	Val	Glu	Lys	Ser	20	25	30	
Ser	Asp	Gly	Pro	Gly	Ala	Ala	Gln	Glu	Pro	Thr	Trp	Leu	Thr	Asp	35	40	45	
Val	Pro	Ala	Ala	Met	Glu	Phe	Ile	Ala	Ala	Thr	Glu	Val	Ala	Val	50	55	60	
Ile	Gly	Phe	Phe	Gln	Asp	Leu	Glu	Ile	Pro	Ala	Val	Pro	Ile	Leu	65	70	75	
His	Ser	Met	Val	Gln	Lys	Phe	Pro	Gly	Val	Ser	Phe	Gly	Ile	Ser	80	85	90	
Thr	Asp	Ser	Glu	Val	Leu	Thr	His	Tyr	Asn	Ile	Thr	Gly	Asn	Thr	95	100	105	
Ile	Cys	Leu	Phe	Arg	Leu	Val	Asp	Asn	Glu	Gln	Leu	Asn	Leu	Glu	110	115	120	
Asp	Glu	Asp	Ile	Glu	Ser	Ile	Asp	Ala	Thr	Lys	Leu	Ser	Arg	Phe	125	130	135	
Ile	Glu	Ile	Asn	Ser	Leu	His	Met	Val	Thr	Glu	Tyr	Asn	Pro	Val	140	145	150	
Thr	Val	Ile	Gly	Leu	Phe	Asn	Ser	Val	Ile	Gln	Ile	His	Leu	Leu	155	160	165	
Leu	Ile	Met	Asn	Lys	Ala	Ser	Pro	Glu	Tyr	Glu	Glu	Asn	Met	His	170	175	180	
Arg	Tyr	Gln	Lys	Ala	Ala	Lys	Leu	Phe	Gln	Gly	Lys	Ile	Leu	Phe	185	190	195	

Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser		
		200					205					210		
Leu	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr
			215						220					225
Glu	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val
			230						235					240
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly
			245						250					255
Leu	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys
			260						265					270

Val Glu Leu

<210> 359
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 359
 ccagcagtgc ccatactcca tagc 24

<210> 360
 <211> 20
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-20
 <223> Synthetic construct.

<400> 360
 tgacgagtgg gatacactgc 20

<210> 361
 <211> 24
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.

<400> 361
 gctctacgga aacttctgct gtgg 24

<210> 362

0
NA
rtificial

<1.1> Artificial Sequence

<1.2> 1-50

<2.3> Synthetic construct.

<400> 362

atctccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<1.1> 363

<2.1> 1777

<2.12> DNA

<2.13> Homo sapiens

<400> 363

ggagagccgc ggctgggacc ggagtgggga gcgcggcgctg gaggtgccac 50
ccggcgcgggg tggcgggagag atcagaagcc tcttcccccac gccgagccaa 100
cctcagcggg gaccgcggct cagggacgcg gcggcgggcg cggcgaactgc 150
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200
cccagacagc cggcgctggc tgtggctcgg gctggcgggc gcgcttgggc 250
tcttgacagc tggagtatca gccttggaag tatatacgcc aaaagaaatc 300
ttcgtggcaa atggtacaca agggaaagctg acctgcaagt tcaagtctac 350
tagtacgact ggcggggtga cctcagtcct ctggagcttc cagccagagg 400
gggccgacac tactgtgtcg ttttccact actcccaagg gcaagtgtac 450
cttggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag tttatacaca 550
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600
cctggacaca ttaggctcta tgcgtagaa aaagagaatt tgctgtgtt 650
tccagtttg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700
ctctgtcat cagcatgatt ctggctgtcc tetatagaag gaaaaactct 750
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800
gcaggctcct cggaagtcac cctccgacac tgagggtctt gtaaagagtc 850
tgcttctgg atctcaccag ggcccagtc tatatgcaca gttagaccac 900
tccggcggac atcacagtga caagattaac aagtcagagt ctgtggtgta 950
tgccgatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

tttttaaacc aaaaactggac tctcgtqcaq aaaatgtagc ccattaccac 1050
 ttttggctt ggagaccacag gcaaggacaa gtacacgtgt actcacagag 1100
 tttttaaag atgtgtacaa aggatatgta taaatattct atttagtcac 1150
 gtttatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200
 ttttcttccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250
 ttttgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300
 tttcttaatg gagacaatag cagatcctgt agtatltcca gtagacatgg 1350
 ccttttaate taagggccta agactgatta gtcttagcat ttactgtagt 1400
 tggaggatgg agatgctatg atggaagcat acccagggig gccttttagca 1450
 cagtatcagt accatttatt tgtctgccgc ttttaaaaaa taccatttgg 1500
 ctatgccact tgaaaacaat ttgagaagtt ttttgaagt ttttctcact 1550
 aaaatatggg gcaattgtta gccttacatg ttgtglagac ttactttaag 1600
 tttgcacctt tgaaatgtgt catatcaatt tctggattca taatagcaag 1650
 attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700
 tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750
 cgtggagagt aaaaagtatc ggtttta 1777

<210> 364
 <211> 269
 <212> PRT
 <213> Homo sapiens

<400> 364
 Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp
 1 5 10 15
 Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu
 20 25 30
 Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu
 35 40 45
 Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe
 50 55 60
 Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser
 65 70 75
 Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr
 80 85 90
 Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp
 95 100 105

Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
		110					115					120
Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
		125					130					135
Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
		140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe
			155						160			165
Thr	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu
			170						175			180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg
			185						190			195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser
			200						205			210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr
			215						220			225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro
			230						235			240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp
			245						250			255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys
			260						265			

<210> 365
 <211> 1321
 <212> DNA
 <213> Homo sapiens

<400> 365
 gccggctgtg cagagacgcc atgtaccggc tccgtgcagc agtgactgcc 50
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggg 100
 ccacagcgc gccgggctgc cgcctctcgg ccacggctgg gtcggggggc 150
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200
 agggggcggg ccccgccgca gtcccccgg gccccgacc ctgaggcgtc 250
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tgggtctccg 300
 agaccccgcc gccgcctgc tccaggtgct tcgccagagc catcgagagc 350
 agccgcgacc tgctgcacag gatcaaggat gaggtggggc caccgggcat 400
 agtggttgga gttctgtag atggaaaaga agtctggtea gaaggtttag 450
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

ttaacta gcatcagcaa aagtcacacc atggttgcctc ttgccaaatt 550
 tttgagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600
 ttttccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650
 ttttaactga ttcccatctt aagtgggaatt cgtcattatg aaaaggacat 700
 ttttgaaggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750
 agt atgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800
 gtt ttaacta aatttlaaac agagcaggag aatgaagcca aatgccggaa 850
 ttttaaaactt ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900
 tgagagaaaaa gtttgaaaat tcaattgaat cctaagatt atttaaaaat 950
 gatcttttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaatatt 1050
 tggactatat gcagaaaaata ttccatgact tggatatgct gacgactgtg 1100
 caggaagaaa acgagccagt gatttacaat agagcaaggt aatgaatac 1150
 cttctgctgt gtctagctat atcgcatctt aacactatctt tattaattaa 1200
 aagtcaaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250
 gagcttttct acatgtctgt tttctcatct glaaagtga ggaagtaaaa 1300
 catgtttata aagtaaaaaa a 1321

<210> 366

<211> 373

<212> PRT

<213> Homo sapiens

<400> 366

Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro
 1 5 10 15

Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg
 20 25 30

Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly
 35 40 45

Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu
 50 55 60

Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu
 65 70 75

Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro
 80 85 90

Trp	Ser	Pro	Gln	Thr	Pro	Ala	Pro	Pro	Cys	Ser	Arg	Cys	Phe	Ala		95	100	105
Arg	Ala	Ile	Glu	Ser	Ser	Arg	Asp	Leu	Leu	His	Arg	Ile	Lys	Asp		110	115	120
Glu	Val	Gly	Ala	Pro	Gly	Ile	Val	Val	Gly	Val	Ser	Val	Asp	Gly		125	130	135
Lys	Glu	Val	Trp	Ser	Glu	Gly	Leu	Gly	Tyr	Ala	Asp	Val	Glu	Asn		140	145	150
Arg	Val	Pro	Cys	Lys	Pro	Glu	Thr	Val	Met	Arg	Ile	Ala	Ser	Ile		155	160	165
Ser	Lys	Ser	Leu	Thr	Met	Val	Ala	Leu	Ala	Lys	Leu	Trp	Glu	Ala		170	175	180
Gly	Lys	Leu	Asp	Leu	Asp	Ile	Pro	Val	Gln	His	Tyr	Val	Pro	Glu		185	190	195
Phe	Pro	Glu	Lys	Glu	Tyr	Glu	Gly	Glu	Lys	Val	Ser	Val	Thr	Thr		200	205	210
Arg	Leu	Leu	Ile	Ser	His	Leu	Ser	Gly	Ile	Arg	His	Tyr	Glu	Lys		215	220	225
Asp	Ile	Lys	Lys	Val	Lys	Glu	Glu	Lys	Ala	Tyr	Lys	Ala	Leu	Lys		230	235	240
Met	Met	Lys	Glu	Asn	Val	Ala	Phe	Glu	Gln	Glu	Lys	Glu	Gly	Lys		245	250	255
Ser	Asn	Glu	Lys	Asn	Asp	Phe	Thr	Lys	Phe	Lys	Thr	Glu	Gln	Glu		260	265	270
Asn	Glu	Ala	Lys	Cys	Arg	Asn	Ser	Lys	Pro	Gly	Lys	Lys	Lys	Asn		275	280	285
Asp	Phe	Glu	Gln	Gly	Glu	Leu	Tyr	Leu	Arg	Glu	Lys	Phe	Glu	Asn		290	295	300
Ser	Ile	Glu	Ser	Leu	Arg	Leu	Phe	Lys	Asn	Asp	Pro	Leu	Phe	Phe		305	310	315
Lys	Pro	Gly	Ser	Gln	Phe	Leu	Tyr	Ser	Thr	Phe	Gly	Tyr	Thr	Leu		320	325	330
Leu	Ala	Ala	Ile	Val	Glu	Arg	Ala	Ser	Gly	Cys	Lys	Tyr	Leu	Asp		335	340	345
Tyr	Met	Gln	Lys	Ile	Phe	His	Asp	Leu	Asp	Met	Leu	Thr	Thr	Val		350	355	360
Gln	Glu	Glu	Asn	Glu	Pro	Val	Ile	Tyr	Asn	Arg	Ala	Arg				365	370	

<210> 367

<210> 30
<211> NA
<212> Artificial

<220>
<221> Artificial Sequence
<222> 1-30
<223> Synthetic construct.

<400> 367
t gaaagaa gtctggtcag aagggttagg 30

<210> 368
<211> 25
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-25
<223> Synthetic construct.

<400> 368
catttggtt cattctctg ctctg 25

<210> 369
<211> 28
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-28
<223> Synthetic construct.

<400> 369
aaaacctcag aacaactcat ttgcacc 28

<210> 370
<211> 41
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-41
<223> Synthetic construct.

<400> 370
gtctcaccat ggttgctctt gccaaattgt gggaagcagg g 41

<210> 371
<211> 1150
<212> DNA
<213> Homo sapiens

<400> 371
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

ggttcgggtt cgaggttggg gggaaagaag cgagatgggg gaagccaggg 100
 ctggggcaac cgggttgggc ctgctcttgc tgatggcggt agcaccggcc 150
 ttttcggccc ggggaacagg ctgcggggcc gggactgggt cgggaagggg 200
 tttttcggaa ggtcgagagg ggcagggctg tggcacgggt gggctgctgc 250
 tggagcactc atttcagatc gatgacagtg ccaacttcgg gaagcggggg 300
 tcaatgctct ggaaccagca ggtatggtacc ttgtccctgt cacacgggca 350
 tctcagcgag gaggagcggg gccgactcgg ggatgtggca gccctgaatg 400
 gctctgaccg ggtccggatc ccaaggcgac cgggggccct ggatggcctg 450
 gaagctgggt gctatgtctc ctctcttgc cctgggtgct ccttgggtga 500
 gtgcacactg tcggaccagc tgaccttgca cgtggatgtg gccggcaacg 550
 tggfgggggt gtcgggtgtg acgcaccccg ggggtgccc gggccatgag 600
 gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650
 gccaccaca gccccagycg ctgagacggc ggccttcatt gaacgcctgg 700
 agatggaaca gggccagaag gcccaagaacc cccaggagca gaagtccttc 750
 ttgcgcaaat actggatgta catcattccc gtcttctgt tctcatgat 800
 gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850
 gtgggtgggg tagtggcctt tctgtgtgc caccctccct gtaagtctat 900
 ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950
 agcttcacgc agccaaaagc aactgttgtt ttggcaagac ggtcctgatg 1000
 tacaagcttg attgaaatc actgctcact tgatacgtta ttcaqaaacc 1050
 caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcaactgtg 1100
 ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
			20						25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
			35						40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	50	55	60
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	65	70	75
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	80	85	90
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	95	100	105
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	110	115	120
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	125	130	135
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	140	145	150
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	155	160	165
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	170	175	180
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	185	190	195
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	200	205	210
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	215	220	225
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	230	235	240
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	245	250	255
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		260	265	

<210> 373

<211> 1706

<212> DNA

<213> Homo sapiens

<400> 373

ggagcgtctgc tggaaaccga gccggagccg gagccacagc ggggagggtg 50

gcctggcggc ctggagccgg acgtgtccgg ggcgtcccg cagaccgggg 100

cagcaggteg tccgggggcc caccatgctg gtgaactgctt accttgcttt 150

tgtaggcctc ctggcctcct gactggggct ggaactgtca agatgcggg 200

...ta cteccatita gaaaataaac actttttaast gatcaaaaaa 1700
 aaaaaa 1706

... 74
 <211> 450
 ... RT
 <213> Homo sapiens

<400> 374
 Met Leu Val Thr Ala Tyr Leu Ala Phe Val Gly Leu Leu Ala Ser
 1 5 10 15
 Cys Leu Gly Leu Glu Leu Ser Arg Cys Arg Ala Lys Pro Pro Gly
 20 25 30
 Arg Ala Cys Ser Asn Pro Ser Phe Leu Arg Phe Gln Leu Asp Phe
 35 40 45
 Tyr Gln Val Tyr Phe Leu Ala Leu Ala Ala Asp Trp Leu Gln Ala
 50 55 60
 Pro Tyr Leu Tyr Lys Leu Tyr Gln His Tyr Tyr Phe Leu Glu Gly
 65 70 75
 Gln Ile Ala Ile Leu Tyr Val Cys Gly Leu Ala Ser Thr Val Leu
 80 85 90
 Phe Gly Leu Val Ala Ser Ser Leu Val Asp Trp Leu Gly Arg Lys
 95 100 105
 Asn Ser Cys Val Leu Phe Ser Leu Thr Tyr Ser Leu Cys Cys Leu
 110 115 120
 Thr Lys Leu Ser Gln Asp Tyr Phe Val Leu Leu Val Gly Arg Ala
 125 130 135
 Leu Gly Gly Leu Ser Thr Ala Leu Leu Phe Ser Ala Phe Glu Ala
 140 145 150
 Trp Tyr Ile His Glu His Val Glu Arg His Asp Phe Pro Ala Glu
 155 160 165
 Trp Ile Pro Ala Thr Phe Ala Arg Ala Ala Phe Trp Asn His Val
 170 175 180
 Leu Ala Val Val Ala Gly Val Ala Ala Glu Ala Val Ala Ser Trp
 185 190 195
 Ile Gly Leu Gly Pro Val Ala Pro Phe Val Ala Ala Ile Pro Leu
 200 205 210
 Leu Ala Leu Ala Gly Ala Leu Ala Leu Arg Asn Trp Gly Glu Asn
 215 220 225
 Tyr Asp Arg Gln Arg Ala Phe Ser Arg Thr Cys Ala Gly Gly Leu
 230 235 240

1	Lys	Leu	Leu	Ser	Asp	Arg	Arg	Val	Leu	Leu	Leu	Gly	Thr	Ile	245	250	255	
	Gln	Ala	Leu	Phe	Glu	Ser	Val	Ile	Phe	Ile	Phe	Val	Phe	Leu	Trp	260	265	270
	Thr	Pro	Val	Leu	Asp	Pro	His	Gly	Ala	Pro	Leu	Gly	Ile	Ile	Phe	275	280	285
	Ser	Ser	Phe	Met	Ala	Ala	Ser	Leu	Leu	Gly	Ser	Ser	Leu	Tyr	Arg	290	295	300
	Ile	Ala	Thr	Ser	Lys	Arg	Tyr	His	Leu	Gln	Pro	Met	His	Leu	Leu	305	310	315
	Ser	Leu	Ala	Val	Leu	Ile	Val	Val	Phe	Ser	Leu	Phe	Met	Leu	Thr	320	325	330
	Phe	Ser	Thr	Ser	Pro	Gly	Gln	Glu	Ser	Pro	Val	Glu	Ser	Phe	Ile	335	340	345
	Ala	Phe	Leu	Leu	Ile	Glu	Leu	Ala	Cys	Gly	Leu	Tyr	Phe	Pro	Ser	350	355	360
	Met	Ser	Phe	Leu	Arg	Arg	Lys	Val	Ile	Pro	Glu	Thr	Glu	Gln	Ala	365	370	375
	Gly	Val	Leu	Asn	Trp	Phe	Arg	Val	Pro	Leu	His	Ser	Leu	Ala	Cys	380	385	390
	Leu	Gly	Leu	Leu	Val	Leu	His	Asp	Ser	Asp	Arg	Lys	Thr	Gly	Thr	395	400	405
	Arg	Asn	Met	Phe	Ser	Ile	Cys	Ser	Ala	Val	Met	Val	Met	Ala	Leu	410	415	420
	Leu	Ala	Val	Val	Gly	Leu	Phe	Thr	Val	Val	Arg	His	Asp	Ala	Glu	425	430	435
	Leu	Arg	Val	Pro	Ser	Pro	Thr	Glu	Glu	Pro	Tyr	Ala	Pro	Glu	Leu	440	445	450

<210> 375

<211> 1098

<212> DNA

<213> Artificial

<400> 375

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gctccccgcg tgcgtcgcg cccacggctt ccgtatccat gattatttgt 150
actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200
cctgccaaag actttggtgg tatctttcac acaaggtatg agcagattca 250

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cctttccccc gctgaaccctc cagagggcctg cggggaacctc agcaacgggtt 300
 tcttcctcca ggaccagatt gctctggttg agaggggggg ctgctccttc 350
 ctcttcaga ctccgggtgt ccaggagcac ggccggccggg cggatgacat 400
 ctcttcacac gcagttgaca atgacagctt ctacgtggag atgatccagg 450
 acagttacca ggcacacgt gacatccccg cctcttctct gctcggccga 500
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<210> 376

<211> 188

<212> PRT

<213> Homo sapiens

<400> 376

Met	Val	Pro	Gly	Ala	Ala	Gly	Trp	Cys	Cys	Leu	Val	Leu	Trp	Leu
1				5					10					15

Pro	Ala	Cys	Val	Ala	Ala	His	Gly	Phe	Arg	Ile	His	Asp	Tyr	Leu
			20						25					30

Tyr	Phe	Gln	Val	Leu	Ser	Pro	Gly	Asp	Ile	Arg	Tyr	Ile	Phe	Thr
			35						40					45

Ala	Thr	Pro	Ala	Lys	Asp	Phe	Gly	Gly	Ile	Phe	His	Thr	Arg	Tyr
			50						55					60

Glu	Gln	Ile	His	Leu	Val	Pro	Ala	Glu	Pro	Pro	Glu	Ala	Cys	Gly
			65						70					75

Glu	Leu	Ser	Asn	Gly	Phe	Phe	Ile	Gln	Asp	Gln	Ile	Ala	Leu	Val
			80						85					90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln
 95 100 105
 Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp
 110 115 120
 Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg
 125 130 135
 Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr
 140 145 150
 Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile
 155 160 165
 Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu
 170 175 180
 Leu Gln Pro Pro Trp Thr Phe Trp
 185

<210> 377
 <211> 496
 <212> DNA
 <213> Artificial

<220>
 <221> unsure
 <222> 396
 <223> unknown base

<400> 377
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 ggctggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100
 ctgaacaaga tggtaagca agtgaactggg aaaatgcccc tectctccta 150
 ctggccctac ggcctgtcact gcggactagg tggcagaggc caacccaaag 200
 atgccacgga ctggtgtctgc cagacccatg actgctgcta tgaccacctg 250
 aagaccacgg ggtgcggcat ctacaaggac aacaacaaaa gcagcataca 300
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378
 <211> 116
 <212> PRT
 <213> Homo sapiens

<400> 378

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccc tctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggccagg agagtataaa 50

agcgatgtgg aggggtgccc gcacaaccag acgcccagtc acaggcgaga 100

gcccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150

ctcctggggg gcccacctg ggcagggaag atgtatggcc ctggaggagg 200

caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250

gggtgtctgt aggtcttctc ctggtgaaaa ggtgccagggt gaaacttgga 300

gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350

cacctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400

ctttcctccg gggatgggc atgtacacca gcaaggaccg ctatttctat 450

tttgggaagc ttgatggca gatctcctct gcctaccca gccaaaggagg 500

gcagggtgctg gtgggcatct atggccagta tcaactcctt ggcatcaaga 550

gcattggcct tgaatggaat tatccactag aggagccgac cactgagcca 600

ccagttaatc tcacatactc agcaaaactca cccgtgggtc gctaggggtg 650

ggtatggggc catccgagct gaggccatct gtgtgggtgt ggtgatggt 700

actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750

gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala Leu
1 5 10 15

Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
20 25 30

Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr
35 40 45

Gly	Leu	Arg	Val	Ser	Val	Gly	Leu	Leu	Leu	Val	Lys	Ser	Val	Gln
				50					55					60
Val	Lys	Leu	Gly	Asp	Ser	Trp	Asp	Val	Lys	Leu	Gly	Ala	Leu	Gly
				65					70					75
Gly	Asn	Thr	Gln	Glu	Val	Thr	Leu	Gln	Pro	Gly	Glu	Tyr	Ile	Thr
				80					85					90
Lys	Val	Phe	Val	Ala	Phe	Gln	Ala	Phe	Leu	Arg	Gly	Met	Val	Met
				95					100					105
Tyr	Thr	Ser	Lys	Asp	Arg	Tyr	Phe	Tyr	Phe	Gly	Lys	Leu	Asp	Gly
				110					115					120
Gln	Ile	Ser	Ser	Ala	Tyr	Pro	Ser	Gln	Glu	Gly	Gln	Val	Leu	Val
				125					130					135
Gly	Ile	Tyr	Gly	Gln	Tyr	Gln	Leu	Leu	Gly	Ile	Lys	Ser	Ile	Gly
				140					145					150
Phe	Glu	Trp	Asn	Tyr	Pro	Leu	Glu	Glu	Pro	Thr	Thr	Glu	Pro	Pro
				155					160					165
Val	Asn	Leu	Thr	Tyr	Ser	Ala	Asn	Ser	Pro	Val	Gly	Arg		
				170					175					

<210> 384
 <211> 2379
 <212> DNA
 <213> Homo sapiens

<400> 384
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 atacagatgt ggcagctcag gtagecccaa attgcctgga agaatacatc 150
 atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200
 cccctcccca ccccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250
 atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300
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 tgtcagcgag cctgactca ctacagtgcg gctgacaggg gctgtcatgc 450
 aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500
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 gggatctgaa cagtttcggg gcttgccgaa gctgctgagt ttacatttac 1000
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 aacctggaac ttttggaactt gggatataac cggatccgaa gtttagccag 1100
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 aatgcagcag aatatattgc tccctgttaa actggctgaa aagtttttaa 1500
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 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650
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 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000
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<210> 385

<211> 513

<212> PRT

<213> Homo sapiens

<400> 385

Met	Gly	Phe	Asn	Val	Ile	Arg	Leu	Leu	Ser	Gly	Ser	Ala	Val	Ala	1	5	10	15
Leu	Val	Ile	Ala	Pro	Thr	Val	Leu	Leu	Thr	Met	Leu	Ser	Ser	Ala	20	25	30	
Glu	Arg	Gly	Cys	Pro	Lys	Gly	Cys	Arg	Cys	Glu	Gly	Lys	Met	Val	35	40	45	
Tyr	Cys	Glu	Ser	Gln	Lys	Leu	Gln	Glu	Ile	Pro	Ser	Ser	Ile	Ser	50	55	60	
Ala	Gly	Cys	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	Ser	Leu	Gln	Lys	65	70	75	
Leu	Lys	Tyr	Asn	Gln	Phe	Lys	Gly	Leu	Asn	Gln	Leu	Thr	Trp	Leu	80	85	90	
Tyr	Leu	Asp	His	Asn	His	Ile	Ser	Asn	Ile	Asp	Glu	Asn	Ala	Phe	95	100	105	
Asn	Gly	Ile	Arg	Arg	Leu	Lys	Glu	Leu	Ile	Leu	Ser	Ser	Asn	Arg	110	115	120	
Ile	Ser	Tyr	Phe	Leu	Asn	Asn	Thr	Phe	Arg	Pro	Val	Thr	Asn	Leu	125	130	135	
Arg	Asn	Leu	Asp	Leu	Ser	Tyr	Asn	Gln	Leu	His	Ser	Leu	Gly	Ser	140	145	150	
Glu	Gln	Phe	Arg	Gly	Leu	Arg	Lys	Leu	Leu	Ser	Leu	His	Leu	Arg	155	160	165	
Ser	Asn	Ser	Leu	Arg	Thr	Ile	Pro	Val	Arg	Ile	Phe	Gln	Asp	Cys	170	175	180	
Arg	Asn	Leu	Glu	Leu	Leu	Asp	Leu	Gly	Tyr	Asn	Arg	Ile	Arg	Ser	185	190	195	
Leu	Ala	Arg	Asn	Val	Phe	Ala	Gly	Met	Ile	Arg	Leu	Lys	Glu	Leu				

200	205	210
Phe Leu Glu His Asn Gln Phe Ser Lys	Leu Asn Leu Ala Leu Phe	
215	220	225
Pro Arg Leu Val Ser Leu Gln Asn Leu Tyr	Leu Gln Trp Asn Lys	
230	235	240
Ile Ser Val Ile Gly Gln Thr Met Ser	Trp Thr Trp Ser Ser Leu	
245	250	255
Gln Arg Leu Asp Leu Ser Gly Asn Glu	Ile Glu Ala Phe Ser Gly	
260	265	270
Pro Ser Val Phe Gln Cys Val Pro Asn	Leu Gln Arg Leu Asn Leu	
275	280	285
Asp Ser Asn Lys Leu Thr Phe Ile Gly	Gln Glu Ile Leu Asp Ser	
290	295	300
Trp Ile Ser Leu Asn Asp Ile Ser Leu	Ala Gly Asn Ile Trp Glu	
305	310	315
Cys Ser Arg Asn Ile Cys Ser Leu Val	Asn Trp Leu Lys Ser Phe	
320	325	330
Lys Gly Leu Arg Glu Asn Thr Ile Ile	Cys Ala Ser Pro Lys Glu	
335	340	345
Leu Gln Gly Val Asn Val Ile Asp Ala	Val Lys Asn Tyr Ser Ile	
350	355	360
Cys Gly Lys Ser Thr Thr Glu Arg Phe	Asp Leu Ala Arg Ala Leu	
365	370	375
Pro Lys Pro Thr Phe Lys Pro Lys Leu	Pro Arg Pro Lys His Glu	
380	385	390
Ser Lys Pro Pro Leu Pro Pro Thr Val	Gly Ala Thr Glu Pro Gly	
395	400	405
Pro Glu Thr Asp Ala Asp Ala Glu His	Ile Ser Phe His Lys Ile	
410	415	420
Ile Ala Gly Ser Val Ala Leu Phe Leu	Ser Val Leu Val Ile Leu	
425	430	435
Leu Val Ile Tyr Val Ser Trp Lys Arg	Tyr Pro Ala Ser Met Lys	
440	445	450
Gln Leu Gln Gln Arg Ser Leu Met Arg	Arg His Arg Lys Lys Lys	
455	460	465
Arg Gln Ser Leu Lys Gln Met Thr Pro	Ser Thr Gln Glu Phe Tyr	
470	475	480
Val Asp Tyr Lys Pro Thr Asn Thr Glu	Thr Ser Glu Met Leu Leu	
485	490	495

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu
500 505 510

Cys Glu Val

<210> 386
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 386
ctgggatctg aacagtttcg gggc 24

<210> 387
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 387
ggtecccagg acatggtctg tccc 24

<210> 388
<211> 48
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-48
<223> Synthetic construct.

<400> 388
gctgaqtta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389
<211> 1449
<212> DNA
<213> Homo sapiens

<400> 389
agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50
ttgactgtcc tttaaataatg tcaagatcca gacttttcag tgtaacctca 100
gcgatctcaa cgaataggat cttgtgtttg ccgatattcc agttgggtgt 150
ctcggacctc ccargcgaag aagatgaaa! gtgtgtaaat tataatgacc 200

metaa tggctgggtat atctggatcc tectgtctgt ggttttgggtg 250
 tggcttctc tctgtggagc tgtggtctct tgcctccagt gctggctgag 300
 tggaga attgattctc acaggcgac catggcagtt tttgtctgtg 350
 tgggtgga ctctatllat gggacagaag cagctgtgag tccaactgtt 400
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 ctgacaaaatt tgttgaacaa aacaataaac atcaatagat atctaaaaa 1449

<210> 390

<211> 146

<212> PRT

<213> Homo sapiens

<400> 390

Met	Ser	Arg	Ser	Arg	Leu	Phe	Ser	Val	Thr	Ser	Ala	Ile	Ser	Thr
1				5				10					15	

1	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
			20					25					30	
2	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln
			35					40					45	
3	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Val	Leu	
			50					55					60	
4	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys
			65					70					75	
5	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala
			80					85					90	
6	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala
			95					100					105	
7	Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr
			110					115					120	
8	Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly
			125					130					135	
9	Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr			
			140					145						

<210> 391

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 391

cttttcagtg tcacctcagc gatctc 26

<210> 392

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 392

ccaaaacatg gagcaggaac agg 23

<210> 393

<211> 47

<212> DNA

<213> Artificial

Artificial Sequence
 1-47
 222 Synthetic construct.

400-393
 ccagttgggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

100-394
 211-2340
 212-DNA
 213-Homo sapiens

100-394
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 gcccaaccggc gttctctcag ctcgatcttg aggcctgttc gccagtgtgg 100
 gacgcagctg acgcccgttt attagctctc gctgcgtcgc ccgggtcag 150
 aagctccgtg gggcgggcga ccgtgacgag aagcccacgg ccagctcagt 200
 tctctttctac ttggggagag agagaaagtc agatgccctt tttaaactcc 250
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 cttagctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350
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 gctctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450
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 1350 actatatttt gttattccaa ttatgagcag agaaaggaaa
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 2150 ctatagtaac tgcttaagtg cagctagctt ctagatttag
 2200 atttagatat tgtattgttc gtcattataa tatgetacca
 2250 taattacaat attttattaa aataaataig tgaaatattg
 2300 gacagalltc caaatctctc ttctcttctc tgaactgtct
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<210> 395

<211> 140

<212> PRT

<213> Homo sapiens

<400> 395

Met	Phe	Phe	Thr	Ile	Ser	Arg	Lys	Asn	Met	Ser	Gln	Lys	Leu	Ser
1				5				10					15	

1. Phe Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu
 20 25 30
 2. Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu
 35 40 45
 3. Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu
 50 55 60
 4. Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser
 65 70 75
 5. Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu
 80 85 90
 6. Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp
 95 100 105
 7. Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr
 110 115 120
 8. Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val
 125 130 135
 9. Ser Gly Ser Ile Arg
 140

<210> 396
 <211> 2639
 <212> DNA
 <213> Homo sapiens

<400> 396
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 acctcgccc ttctgacag ctccagcctg actcgggtgg attgtagcgg 200
 cctgggcccc caccatcatg cggtgcccat cctctggac acagcccact 250
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 gggccgggct acacgacgtt ggtggcctg gatctcagcc acaacctgt 350
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2639

<210> 397

<211> 353

<212> PRT

<213> Homo sapiens

<400> 397

Met	Pro	Trp	Pro	Leu	Leu	Leu	Leu	Ala	Val	Ser	Gly	Ala	Gln
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Thr	Thr	Arg	Pro	Cys	Phe	Pro	Gly	Cys	Gln	Cys	Glu	Val	Glu
			20					25					30
Phe	Gly	Leu	Phe	Asp	Ser	Phe	Ser	Leu	Thr	Arg	Val	Asp	Cys
			35					40					45
Gly	Leu	Gly	Pro	His	Ile	Met	Pro	Val	Pro	Ile	Pro	Leu	Asp
			50					55					60
Ala	His	Leu	Asp	Leu	Ser	Ser	Asn	Arg	Leu	Glu	Met	Val	Asn
			65					70					75
Ser	Val	Leu	Ala	Gly	Pro	Gly	Tyr	Thr	Thr	Leu	Ala	Gly	Leu
			80					85					90
Leu	Ser	His	Asn	Leu	Leu	Thr	Ser	Ile	Ser	Pro	Thr	Ala	Phe
			95					100					105
Arg	Leu	Arg	Tyr	Leu	Glu	Ser	Leu	Asp	Leu	Ser	His	Asn	Gly
			110					115					120
Thr	Ala	Leu	Pro	Ala	Glu	Ser	Phe	Thr	Ser	Ser	Pro	Leu	Ser
			125					130					135
Val	Asn	Leu	Ser	His	Asn	Gln	Leu	Arg	Glu	Val	Ser	Val	Ser
			140					145					150

Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser	155	160	165
His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly	170	175	180
Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg	185	190	195
Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu	200	205	210
Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe	215	220	225
Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln	230	235	240
Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly	245	250	255
Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala	260	265	270
Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp	275	280	285
Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu	290	295	300
His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg	305	310	315
Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly	320	325	330
Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser	335	340	345
Ala Ala Arg Gly Pro Thr Ile Leu	350		

<210> 398

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 398

ccctgccagc cgagagcttc acc 23

<210> 399

<211> 23

<212> DNA

<21> Artificial

<20>

<21> Artificial Sequence

<22> 1-23

<23> Synthetic construct.

<400> 399

gatttggtgcc cgaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

gattggcgag ccacagcttc tgtgagattc gattttctccc cagttccct 50

gtgggtctga ggggaccaga agggtagct acgttggctt tctggaagg 100

gaggetatat gcgtcaatc cccaaaacaa gttttgacat ttccctgaa 150

atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200

ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250

cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300

ttctcttcac gggaggettg gcagtttttc ttactcctgt ggtctccaga 350

tttcaggcct aagatgaaag cctctagctt tgccttcagc ctctctctctg 400

ctgcgtttta tctctatgg actccttcca ctggactgaa gacactcaat 450

ttgggaagct gtgtgatcgc cacaaacctt caggaaatac gaaatggatt 500

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tgttgcctcc tgcgccattt gctaagactc tatctggaca ggtatttaa 650

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ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

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 aatctacac gccagcatg tattctaca aataaagttt tctttgcata 1550
 ccaaaaaaaaa aaaaaaaaaa a 1571

<210> 402

<211> 261

<212> PRT

<213> Homo sapiens

<400> 402

Met	Arg	Gln	Phe	Pro	Lys	Thr	Ser	Phe	Asp	Ile	Ser	Pro	Glu	Met
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Ser	Phe	Ser	Ile	Tyr	Ser	Leu	Gln	Val	Pro	Ala	Val	Pro	Gly	Leu
			20						25				30	
Thr	Cys	Trp	Ala	Leu	Thr	Ala	Glu	Pro	Gly	Trp	Gly	Gln	Asn	Lys
			35						40				45	
Gly	Ala	Thr	Thr	Cys	Ala	Thr	Asn	Ser	His	Ser	Asp	Ser	Glu	Leu
			50						55				60	
Arg	Pro	Glu	Ile	Phe	Ser	Ser	Arg	Glu	Ala	Trp	Gln	Phe	Phe	Leu
			65						70				75	
Leu	Leu	Trp	Ser	Pro	Asp	Phe	Arg	Pro	Lys	Met	Lys	Ala	Ser	Ser
			80						85				90	

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr	95	100	105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile	110	115	120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg	125	130	135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu	140	145	150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys	155	160	165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe	170	175	180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser	185	190	195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu	200	205	210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys	215	220	225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln	230	235	240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln	245	250	255
Trp	Met	Glu	Glu	Thr	Glu										260		

<210> 403

<211> 28

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-28

<223> Synthetic construct.

<400> 403

ctcctgtggt ctccagattt caggccta 28

<210> 404

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<209> 404
<210> 405

<211> 323
<212> PRT

<213> Homo sapiens

<210> 405
cggcctatcgt cttgcgcctac tgcctgaatgt ccgtcccggga ggaggaggag 50
aggccttttgc cgcctgaccca gagatggccc cgagcgcagca aattcctact 100
ctccgggtgc gggtctaccg tggccgagct agcaaccttt cccctggatc 150
tcacaaaaaac tcgactccaa atgcaaggag aagcagctct tgcctcggttg 200
ggagacgggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300
caccgcgccat ttacagacac gtagtgtatt ctggaggctcg aatggtcaca 350
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400
tccccctttgg aaatcagtca ttggagggat gatggctggf gttattggcc 450
agttttttagc caatccaact gacctagtga aggttcagat gcaaattggaa 500
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cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850
ctgccttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900
gctttttacc atcttggtg agaatgaccc cttgggtcaat ggtgttcttg 950
cttacttatg aaaaaatcag agagatgagt ggaqtcagtc cattttaa 998

<210> 406
<211> 323
<212> PRT
<213> Homo sapiens

<400> 406
Met Ser Val Pro Glu Glu Glu Glu Arg Leu Leu Pro Leu Thr Gln
1 5 10 15

Asp	Trp	Pro	Arg	Ala	Ser	Lys	Phe	Leu	Leu	Ser	Gly	Cys	Ala	Ala	
				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Met Ser Gly Val Ser Pro Phe
320

<210> 407

<211> 31

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-31

<223> Synthetic construct.

<400> 407

cgccgcatccc gttatcgtct tgcgctactg c 31

<210> 408

<211> 34

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-34

<223> Synthetic construct.

<400> 408

gcqqaattct taaaatggac tgactccact catc 34

<210> 409

<211> 1487

<212> DNA

<213> Homo sapiens

<400> 409

cggacgcgtg ggcgcgggac gccgcaggg ttgtggcgca gcagtctctt 50

tcttgcgcgc gcgcctgaag tcggcgtggg cgtttgagga agctgggata 100

cagcatttaa tgaaaaatct atgcttaaga agtaaaaaatg gcaggcttcc 150

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agaaatgctg tggcatctgt tgcgcaggt atattgtttt ttacagcctg 250

qtggataatg attgatgcag ctgtggtgta tcctaaacca gaacagttga 300

accatgcctt tcacacatgt ggtgtatctt ccacattggc tttcttcatt 350

ataaatgctg tatccaatgc tcagggtgaga ggtgatagct atgaaagcgg 400

ctgttttaga agaacaggtg ctgcagtttg gcttttcatt ggttttcatt 450

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gttaccctaaa atactgatgt ttatccggga ctacctgtgt tttttcaaaa 550

380

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<210> 410

<211> 158

<212> PRT

<213> Homo sapiens

<400> 410

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Ile	Asp	Trp	Ser	Glu	Arg	Arg	Asn	Ala	Val	Ala	Ser	Val	Val	Ala
				20					25					30
Gly	Ile	Leu	Phe	Phe	Thr	Gly	Trp	Trp	Ile	Met	Ile	Asp	Ala	Ala
				35					40					45
Val	Val	Tyr	Pro	Lys	Pro	Glu	Gln	Leu	Asn	His	Ala	Phe	His	Thr
				50					55					60
Cys	Gly	Val	Phe	Ser	Thr	Leu	Ala	Phe	Phe	Met	Ile	Asn	Ala	Val
				65					70					75

1 r Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu
 80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu
 95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala
 110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe
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Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe
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<210> 411
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 <213> Artificial

<220>
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 <222> 1-20
 <223> Synthetic construct.

<400> 411
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<210> 412
 <211> 20
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<220>
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 <222> 1-20
 <223> Synthetic construct.

<400> 412
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<210> 413
 <211> 40
 <212> DNA
 <213> Artificial

<220>
 <221> Artificial Sequence
 <222> 1-40
 <223> Synthetic construct.

<400> 413
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<210> 414

1337
NA
213 homo sapiens

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actgcattcta qaggagggcc gtctgtgagg ccactacccc tccagcaact 150
qqaaqgtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200
gggcctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250
aagtqqgagc ctcgagccct cgggtlgaag ctgaccccaa gccacccttc 300
acctggacag gatgagagtg tcaggtgtgc ttgcctctct ggccctcacc 350
tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400
catgaaaacc atccgtctgc cagcttgctt ggcagcctcg cccaccaagg 450
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4 5
4
4 16 100
H. sapiens

<400> 416

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	Ile	Val	Thr	Thr	Trp	Met	Phe	Ile	Arg	Ser	Tyr	Met	Ser	Phe	Ser
					20					25					30
	Met	Lys	Thr	Ile	Arg	Leu	Pro	Arg	Trp	Leu	Ala	Ala	Ser	Pro	Thr
					35					40					45
	Lys	Glu	Ile	Gln	Val	Lys	Lys	Tyr	Lys	Cys	Gly	Leu	Ile	Lys	Pro
					50					55					60
	Cys	Pro	Ala	Asn	Tyr	Phe	Ala	Phe	Lys	Ile	Cys	Ser	Gly	Ala	Ala
					65					70					75
	Asn	Val	Val	Gly	Pro	Thr	Met	Cys	Phe	Glu	Asp	Arg	Met	Ile	Met
					80					85					90
	Ser	Pro	Val	Lys	Asn	Asn	Val	Gly	Arg	Gly	Leu	Asn	Ile	Ala	Leu
					95					100					105
	Val	Asn	Gly	Thr	Thr	Gly	Ala	Val	Leu	Gly	Gln	Lys	Ala	Phe	Asp
					110					115					120
	Met	Tyr	Ser	Gly	Asp	Val	Met	His	Leu	Val	Lys	Phe	Leu	Lys	Glu
					125					130					135
	Ile	Pro	Gly	Gly	Ala	Leu	Val	Leu	Val	Ala	Ser	Tyr	Asp	Asp	Pro
					140					145					150
	Gly	Thr	Lys	Met	Asn	Asp	Glu	Ser	Arg	Lys	Leu	Phe	Ser	Asp	Leu
					155					160					165
	Gly	Ser	Ser	Tyr	Ala	Lys	Gln	Leu	Gly	Phe	Arg	Asp	Ser	Trp	Val
					170					175					180
	Phe	Ile	Gly	Ala	Lys	Asp	Leu	Arg	Gly	Lys	Ser	Pro	Phe	Glu	Gln
					185					190					195
	Phe	Leu	Lys	Asn	Ser	Pro	Asp	Thr	Asn	Lys	Tyr	Glu	Gly	Trp	Pro
					200					205					210
	Glu	Leu	Leu	Glu	Met	Glu	Gly	Cys	Met	Pro	Pro	Lys	Pro	Phe	
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<210> 416

<211> 21

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<210> 1-21
 <211> Synthetic construct.
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-21
 <223> Synthetic construct.
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 <210> 417
 <211> 18
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-18
 <223> Synthetic construct.
 <400> 417
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 <210> 418
 <211> 26
 <212> DNA
 <213> Artificial
 <220>
 <221> Artificial Sequence
 <222> 1-26
 <223> Synthetic construct.
 <400> 418
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 <210> 419
 <211> 24
 <212> DNA
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 <220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic construct.
 <400> 419
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 <210> 420
 <211> 24
 <212> DNA
 <213> Artificial
 <220>
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 <222> 1-24
 <223> Synthetic construct.
 <400> 420
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<210> 421
<211> 46
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-46
<223> Synthetic construct.

<400> 421
gtacaagtgt ggcoctcatca agccctgccc agccaactac ttigcg 46

<210> 422
<211> 1701
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1528
<223> unknown base

<400> 422
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caagccagga gctcgctcgc tctctctctc tctctctcac tctctcctcc 200
ctctctctct gctgtctcta gtctcttagt cctcaaattc ccagtcacct 250
gcaccccttc ctgggacact atgttgttct ccgcccctct gctggagggtg 300
atttggaacc tggctgcaga tgggggtcaa cactggacgt atgagggccc 350
acatggtcag gaccattggc cagcctctta ccttgagtgt ggaaacaatg 400
cccagtcgcc catcgatatl cagacagaca gtgtgacatt tgacctgat 450
ttgctgtctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500
ggacctgcac aacaatggcc acacagtgca actctctctg cctctaccc 550
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cactggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650
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 tttccctaga tatactgagg gatctctct taggataaag agttgctgtt 1650
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 t 1701

<210> 423
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 423
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 20 25 30
 Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln
 35 40 45
 Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp
 50 55 60
 Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu
 65 70 75
 Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80										85					90				
Pro	Ser	Thr	Leu	Tyr	Leu	Gly	Gly	Leu	Pro	Arg	Lys	Tyr	Val	Ala					
95										100					105				
Ala	Gln	Leu	His	Leu	His	Trp	Gly	Gln	Lys	Gly	Ser	Pro	Gly	Gly					
110										115					120				
Pro	Glu	His	Gln	Ile	Asn	Ser	Glu	Ala	Thr	Phe	Ala	Glu	Leu	His					
125										130					135				
Ile	Val	His	Tyr	Asp	Ser	Asp	Ser	Tyr	Asp	Ser	Leu	Ser	Glu	Ala					
140										145					150				
Ala	Glu	Arg	Pro	Gln	Gly	Leu	Ala	Val	Leu	Gly	Ile	Leu	Ile	Glu					
155										160					165				
Val	Gly	Glu	Thr	Lys	Asn	Ile	Ala	Tyr	Glu	His	Ile	Leu	Ser	His					
170										175					180				
Leu	His	Glu	Val	Arg	His	Lys	Asp	Gln	Lys	Thr	Ser	Val	Pro	Pro					
185										190					195				
Phe	Asn	Leu	Arg	Glu	Leu	Leu	Pro	Lys	Gln	Leu	Gly	Gln	Tyr	Phe					
200										205					210				
Arg	Tyr	Asn	Gly	Ser	Leu	Thr	Thr	Pro	Pro	Cys	Tyr	Gln	Ser	Val					
215										220					225				
Leu	Trp	Thr	Val	Phe	Tyr	Arg	Arg	Ser	Gln	Ile	Ser	Met	Glu	Gln					
230										235					240				
Leu	Glu	Lys	Leu	Gln	Gly	Thr	Leu	Phe	Ser	Thr	Glu	Glu	Glu	Pro					
245										250					255				
Ser	Lys	Leu	Leu	Val	Gln	Asn	Tyr	Arg	Ala	Leu	Gln	Pro	Leu	Asn					
260										265					270				
Gln	Arg	Met	Val	Phe	Ala	Ser	Phe	Ile	Gln	Ala	Gly	Ser	Ser	Tyr					
275										280					285				
Thr	Thr	Gly	Glu	Met	Leu	Ser	Leu	Gly	Val	Gly	Ile	Leu	Val	Gly					
290										295					300				
Cys	Leu	Cys	Leu	Leu	Leu	Ala	Val	Tyr	Phe	Ile	Ala	Arg	Lys	Ile					
305										310					315				
Arg	Lys	Lys	Arg	Leu	Glu	Asn	Arg	Lys	Ser	Val	Val	Phe	Thr	Ser					
320										325					330				
Ala	Gln	Ala	Thr	Thr	Glu	Ala													
335																			

<210> 424
 <211> 18
 <212> DNA
 <213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 424
gtaaagtcgc tggccagc 18

<210> 425
<211> 18
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-18
<223> Synthetic construct.

<400> 425
cccgatctgc ctqctgta 18

<210> 426
<211> 24
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-24
<223> Synthetic construct.

<400> 426
ctgcactgta tggccattat tgtg 24

<210> 427
<211> 45
<212> DNA
<213> Artificial

<220>
<221> Artificial Sequence
<222> 1-45
<223> Synthetic construct.

<400> 427
cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428
<211> 1073
<212> DNA
<213> Homo sapiens

<400> 428
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gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

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      tttt gggactccct cccacaaaac tggctccgga tcagggaaca 200
      aacccaaacc aacagcagtc aaatcaggtc ttcccttctt taagtctgat 250
      tttt taca cagatgctca cactggggcc agatctgcat ctgttaaate 300
      cgttgagg aatgacacct ggtaccaga cccacccatt gacctggga 350
      tggtttatg tacaacagca actgcacca catgtgttac caattttgt 400
      cccacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450
      aatcttcac gagccctcct atccattcct tgttccggg aggcacctg 500
      cccccagtc aggcaggggc taatccagat gtccaggatg gaagccttc 550
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      gattgagaca cattggatag tcttagaaga aattaattct taatttacct 850
      gaaaatatc ttgaaatttc agaaaatatg ttctatgtag agaateccaa 900
      cttttaaaaa caataattca atggataaat ctgtcttga aatataacat 950
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<210> 429

<211> 209

<212> PRT

<213> Homo sapiens

<400> 429

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Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys
20             25             30

Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn
35             40             45

Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu
50             55             60

Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met
65             70             75

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Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
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				200					205					

<210> 430

<211> 1257

<212> DNA

<213> Homo Sapien

<400> 430

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ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150
gccccgcgcg ctccccgcag cggctcccg gctcctgct gctcctgctg 200
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aaaggcgag ctccggcaga gggaggtygt ggacctgtat aatggaatgt 300
gcttacaagg gccagcagga gtgcctggtc gagacgggag cctggggcc 350
aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400
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actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500
aaaattgcgg agtgtacatt tacaaagatg cgttcaaata gtgctctaag 550
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agcgttggtg attcacattc aatggagctg aatgttcagg acctcttccc 650

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 aattaatatt catgcacatt ctctctgiga aggaactttgt gaaggaattg 750
 gtagtgatt agtggatgtt gctatctggg ttggcacttg ttcagattac 800
 ccaaaaggag atgttctac tggatggaat tcagttctc gcatcattat 850
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<210> 431

<211> 243

<212> PRT

<213> Homo Sapien

<400> 431

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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Leu	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Leu	Pro	Ala	Pro	Ser	Ser	Ala
				20					25					30
Ser	Glu	Ile	Pro	Lys	Gly	Lys	Gln	Lys	Ala	Gln	Leu	Arg	Gln	Arg
				35					40					45
Glu	Val	Val	Asp	Leu	Tyr	Asn	Gly	Met	Cys	Leu	Gln	Gly	Pro	Ala
				50					55					60
Gly	Val	Pro	Gly	Arg	Asp	Gly	Ser	Pro	Gly	Ala	Asn	Val	Ile	Pro
				65					70					75
Gly	Thr	Pro	Gly	Ile	Pro	Gly	Arg	Asp	Gly	Phe	Lys	Gly	Glu	Lys
				80					85					90
Gly	Glu	Cys	Leu	Arg	Glu	Ser	Phe	Glu	Glu	Ser	Trp	Thr	Pro	Asn
				95					100					105
Tyr	Lys	Gln	Cys	Ser	Trp	Ser	Ser	Leu	Asn	Tyr	Gly	Ile	Asp	Leu
				110					115					120
Gly	Lys	Ile	Ala	Glu	Cys	Thr	Phe	Thr	Lys	Met	Arg	Ser	Asn	Ser
				125					130					135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	
				140					145					150	
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	
				155					160					165	
Tyr	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	
				170					175					180	
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	
				185					190					195	
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	
				200					205					210	
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	
				215					220					225	
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Artificial oligonucleotide probe

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